

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:42:12 ; Search time 60.37 Seconds
(without alignments)
15.917 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	75.4	274	2 B84930	H+-transporting ATP hypothetical prote
2	38	66.7	65	2 S38469	conserved hypothetical prote
3	38	66.7	408	2 C82178	hypothetical prote
4	38	66.7	478	2 T25899	protein F3M18.12
5	38	66.7	996	2 F86410	T-cell receptor be
6	37	64.9	113	2 I38320	conserved hypothetical prote
7	37	64.9	196	2 AE2876	hypothetical prote
8	37	64.9	198	2 G97652	hypothetical prote
9	37	64.9	365	1 B64228	hypothetical prote
10	36	63.2	137	2 D58723	hypothetical prote
11	36	63.2	193	2 E65090	hypothetical prote
12	36	63.2	193	2 F85963	hypothetical prote
13	36	63.2	193	2 G91118	conserved hypothetical prote
14	36	63.2	193	2 AF0889	hypothetical prote
15	36	63.2	288	2 G90368	brain and reproduc
16	36	63.2	383	2 JC2472	TPS3 protein - yea
17	36	63.2	1054	2 S54473	hypothetical prote
18	36	63.2	1070	2 S46755	E5 protein - human
19	35.5	62.3	83	1 W5WLHS	succinate dehydrog
20	35	61.4	142	2 C822728	protein F27J15.18
21	35	61.4	224	2 G96527	Fc-gamma receptor
22	35	61.4	270	2 A34636	hypothetical prote
23	35	61.4	299	2 S73406	NADH dehydrogenase
24	35	61.4	316	2 S50336	hypothetical prote
25	35	61.4	380	2 A83458	glycolate oxidase
26	35	61.4	483	2 T03909	proline-rich prote
27	35	61.4	492	2 S74338	hypothetical prote
28	35	61.4	577	2 T09024	hypothetical prote
29	35	61.4	612	2 T39684	hypothetical prote

ALIGNMENTS

RESULT	1	B84930 H+-transporting ATP synthase (EC 3.6.1.34) A chain [imported] - Buchnera sp. (strain C; Species: Buchnera sp. C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 24-Aug-2001 C; Accession: B84930 R; Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H. Nature 407, 81-86, 2000 A; Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A; Reference number: A84930; MUID:20445173 A; Accession: B84930 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-274 <STO> A; Cross-references: GB:AP000398; GSPDB:GN00144 A; Experimental source: strain APS C; Genetics: A; Gene: atpB; BU002 C; Superfamily: H+-transporting ATP synthase protein 6 C; Keywords: hydrolase						
Qy	1 LLMWITQCFL 10			0;	Gaps	0;	Query Match Best Local Similarity 75.4%; Pred. No. 80.0%; Mismatches 0; Indels 2;	
Db	229 LLPWWTQCFL 238			0;	Gaps	0;	Matches 8; Conservative 0; Mismatches 0; Indels 2;	
Qy	1 LLMWITQCFL 10			0;	Gaps	0;	Query Match Best Local Similarity 75.4%; Pred. No. 80.0%; Mismatches 0; Indels 2;	
Db	229 LLPWWTQCFL 238			0;	Gaps	0;	Matches 8; Conservative 0; Mismatches 0; Indels 2;	

QY 1 LLMWITQCF1 10
Db 1 :|||
Db 6 LTMWYARCFL 15

RESULT 3
C82178 conserved hypothetical protein VC1609 [imported] - vibrio cholerae (strain N16961 serogroup C; Species: Vibrio cholerae C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C; Accession: C82178 R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. L., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000 A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A82035; MUID:20406833 A; Accession: C82178 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-408 <HEI> A; Cross-references: GB:AE004239; GB:AE003852; NID:99656130; PIDN:AAF94763.1; GSPDB:GN001 A; Experimental source: serogroup O1; strain N16961; biotype El Tor C; Genetics: A; Gene: VC1609 A; Map position: 1

Query Match 66.7%; Score 38; DB 2; Length 408;
Best Local Similarity 62.5%; Pred. No. 32;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 6
I38320 T-cell receptor beta chain V region (V-beta 26, germline) precursor - human (fragment C; Species: Homo sapiens (man) C; Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Jan-2000 C; Accession: I38320 R; Slightom, J.L.; Siemieniak, D.R.; Sieu, L.C.; Koop, B.F.; Hood, L. Genomics 20, 149-168, 1994 A; Title: Nucleotide sequence analysis of 77.7 kb of the human V beta T-cell receptor A; Reference number: A54302; MUID:94292194 A; Accession: I38320 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-113 <RES> A; Cross-references: EMBL:U03115; NID:9467918; PIDN:AAA17719.1; PID:q467929 C; Genetics: A; Gene: TCRBV26S1 A; Introns: 17/1 C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: T-cell receptor F; 35-113/Domain: immunoglobulin homology <IMM>

Query Match 64.9%; Score 37; DB 2; Length 113;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 7
AE2876 conserved hypothetical protein Atu2439 [imported] - Agrobacterium tumefaciens (strain C; Species: Agrobacterium tumefaciens C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C; Accession: AE2876 R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wooger, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, C; Species: Arabidopsis thaliana (mouse-ear cress) ; Karp, P.; Romero, P.; Zhang, S.

QY 2 LLMWITQCF 9
Db 1 :|||
Db 43 LLWINQCY 50

RESULT 5
F86410 Query Match 66.7%; Score 38; DB 2; Length 478;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LLMWITQCF 9
Db 1 :|||
Db 5 LLCWVTLCLL 14

Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Accession: AB2577; PMID:11743193
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-196 <KUR>
 A;Cross-references: GB:AE0008688; PIDN:AAU43427.1; PID:g17740928; GSPDB:GN00186
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atu2439
 A;Map position: circular chromosome

Query Match 64.9%; Score 37; DB 2; Length 196;
 Best Local Similarity 66.7%; Pred. No. 25;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 LLMWITQCF 9
 |:||:|
 Db 24 LLMWVTPAF 32

RESULT 8
 G97652 hypothetical protein AGR_C_4424 [imported] - Agrobacterium tumefaciens (strain C58, Cere C;Species: Agrobacterium tumefaciens C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 C;Accession: G97652
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A;Reference number: A97359; PMID:11743194
 A;Accession: G97652
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-198 <KUR>
 A;Cross-references: GB:AE007869; PIDN:AAK88176.1; PID:g15157620; GSPDB:GN00169
 C;Genetics:
 A;Gene: AGR_C_4424
 A;Map position: circular chromosome

Query Match 64.9%; Score 37; DB 2; Length 198;
 Best Local Similarity 66.7%; Pred. No. 25;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 LLMWITQCF 9
 |:||:|
 Db 26 LLMWVTPAF 34

RESULT 9
 B64228 hypothetical protein MG255 - Mycoplasma genitalium C;Species: Mycoplasma genitalium C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999 C;Accession: B64228
 R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.C.; Venter, J.C.
 Science 270, 397-403, 1995
 A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-365 <TIGR>
 A;Cross-references: GB:U339703; GB:L43967; NID:g1045933; PID:g1045946; TIGR:MG255
 A;Experimental source: strain G-37

C;Genetics:
 A;Genetic code: SG3
 C;Superfamily: Mycoplasma hypothetical protein MG255

Query Match 64.9%; Score 37; DB 1; Length 365;
 Best Local Similarity 55.6%; Pred. No. 43;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 LMWITQCFL 10
 |:||:
 Db 117 LLWLROCWL 125

RESULT 10
 D58723 hypothetical protein (orf4, cpdA 5' region) - Escherichia coli C;Species: Escherichia coli C;Date: 18-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 20-Feb-1998 C;Accession: D58723
 R;Imamura, R.; Yamanaka, K.; Ogura, T.; Hiraga, S.; Fujita, N.; Ishihama, A.; Niki, H. J. Biol. Chem. 271, 25423-25429, 1996
 A;Title: Identification of the cpdA gene encoding cyclic 3',5'-adenosine monophosphate A;Reference number: A58723; MUID:96411758
 A;Accession: D58723
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-137 <TIGR>
 A;Cross-references: GB:D16557; NID:g453393
 A;Experimental source: strain K-12
 C;Genetics:
 A;Map position: 68.4 min

Query Match 63.2%; Score 36; DB 2; Length 137;
 Best Local Similarity 57.1%; Pred. No. 27;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 WITQCFL 10
 |:||:
 Db 77 WLSQCFM 83

RESULT 11
 E65090 hypothetical 15.2 kd protein in icc 3' region - Escherichia coli (strain K-12) C;Species: Escherichia coli C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999 C;Accession: E65090
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: A64720; MUID:97426617
 A;Accession: E65090
 A;Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-193 <BLAT>
 A;Cross-references: GB:AE000385; GB:U00096; NID:g1789405; PID:g17894
 A;Experimental source: strain K-12, substrain MG1655
 C;Genetics:
 A;Gene: yqIA

Query Match 63.2%; Score 36; DB 2; Length 193;
 Best Local Similarity 57.1%; Pred. No. 37;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 WITQCFL 10
 |:||:
 Db 77 WLSQCFM 83

RESULT 12
F85963 hypothetical protein yqIA [imported] - Escherichia coli (strain O157:H7, substrate EDL93
C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C; Accession: F85963
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, R.; Apodaca,
Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-193 <STOP>
A; Cross-references: GB:AE005174; NID:q12517609; PIDN:AAG58170.1; GSPDB:GN00145; UWGP:Z43
A; Experimental source: strain O157:H7, substrate EDL933
C; Genetics:
A; Gene: yqIA

Query Match 63.2%; Score 36; DB 2; Length 193;
Best Local Similarity 57.1%; Pred. No. 37;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 4 WITQCFL 10
Db 77 WLSQCFM 83

RESULT 13
G91118 hypothetical protein ECs3919 [imported] - Escherichia coli (strain O157:H7, substrate RI
C; Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C; Accession: G91118
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Accession: G91118
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-193 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB37342.1; PID:q133363392; GSPDB:GN00154
A; Experimental source: strain O157:H7, substrate RIMD 0509952
C; Genetics:
A; Gene: ECs3919

Query Match 63.2%; Score 36; DB 2; Length 193;
Best Local Similarity 57.1%; Pred. No. 37;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Qy 4 WITQCFL 10
Db 77 WLSQCFM 83

Search completed: July 16, 2002, 07:48:18
Job time: 366 sec

RESULT 14
AF0889 hypothetical protein STY3360 [imported] - Salmonella enterica subsp. enterica
C; Species: Salmonella enterica subsp. enterica serovar Typhi
A; Note: this species has also been called Salmonella typhi
C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C; Accession: AF0889
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davies, P.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A; Reference number: AB0502; PMID:11677608
A; Accession: AF0889
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-193 <PAR>
A; Cross-references: GB:AL513382; PIDN:CAD03014.1; PID:q16504259; GSPDB:GN00176
C; Genetics:
A; Gene: STY3360

Query Match 63.2%; Score 36; DB 2; Length 193;
Best Local Similarity 57.1%; Pred. No. 37;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WITQCFL 10
Db 77 WLSQCFM 83

RESULT 15
G90368 hypothetical protein acsA-4 [imported] - Sulfolobus solfataricus
C; Species: Sulfolobus solfataricus
C; Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C; Accession: G90368
R; She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Ch
Jong, I.; Jeffries, A.C.; Kozena, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: G90368
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-288 <KUR>
A; Cross-references: GB:AE006641; NID:q13815300; PIDN:AAK42206.1; GSPDB:GN00155
C; Genetics:
A; Gene: acsA-4

Query Match 63.2%; Score 36; DB 2; Length 288;
Best Local Similarity 55.6%; Pred. No. 52;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LMWITQCFL 10
Db 280 LLYITQCYM 288

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Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

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Dr. Link _____

Date Completed: _____

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Patent Family _____

WWW/Internet _____

Online Time: _____

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Other (specify) _____

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 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

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 Sequence Systems _____
 WWW/Internet _____
 Other (specify) _____

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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:47:02 ; Search time 32.19 Seconds
(without alignments)
12.028 Million cell updates/sec

Title: US-09-165-546A-7

Perfect score: 57

Sequence: 1 LIMWITQCFL 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	57	100.0	180	1	CTAG_HUMAN	P78358	homo sapien
2	43	75.4	274	1	ATP6_BUCA1	P57118	buchnera ap
3	37	64.9	365	1	Y255_MYCGE	P47497	mycoplasma
4	36	63.2	193	1	YQIA_ECOLI	P36653	escherichia
5	36	63.2	351	1	VOD1_ARATH	Q91151	arabidopsis
6	36	63.2	351	1	VOD2_ARATH	Q91ha4	arabidopsis
7	36	63.2	1022	1	TPS3_YEAST	P38426	saccharomyces
8	36	63.2	1070	1	YHV4_YEAST	P38850	saccharomyces
9	35.5	62.3	83	1	VE5 HPV16	P06927	human papill
10	35	61.4	299	1	Y060_MYCPN	P75042	mycoplasma
11	35	61.4	341	1	FCG2_CAVPO	Q60513	cavia porce
12	35	61.4	1950	1	UBR1_YEAST	P19812	saccharomyces
13	35	61.4	2103	1	RRPL_UUK	P33453	uukuniemi v
14	34	59.6	132	1	TVC3_MOUSE	P06324	mus musculu
15	34	59.6	135	1	TYC1_MOUSE	P01740	mus musculu
16	34	59.6	219	1	DCK1_FOWPV	P21974	fowlpox vir
17	34	59.6	353	1	YRRI_BACSU	Q34472	bacillus su
18	34	59.6	385	1	YEHY_ECOLI	P33361	escherichia
19	34	59.6	495	1	ACHP_RAT	P12392	rattus norv
20	34	59.6	504	1	PSD3_CAEEL	Q04908	caenorhabdi
21	34	59.6	1502	1	MRP6_RAT	Q88269	rattus norv
22	34	59.6	1503	1	MRP6_HUMAN	Q95255	homo sapien
23	34	59.6	2670	1	IP3T_RAT	Q63269	rattus norv
24	34	59.6	2671	1	IP3T_HUMAN	Q14573	homo sapien
25	33	57.9	114	1	APR2_HUMAN	Q9Y5m1	homo sapien
26	33	57.9	215	1	CIB3_HUMAN	Q9ny72	homo sapien
27	33	57.9	255	1	FOL1_MOUSE	P35846	mus musculu
28	33	57.9	276	1	HEMX_BACSU	P16645	bacillus su
29	33	57.9	345	1	C5AR_CAVPO	Q70129	cavia porce
30	33	57.9	375	1	AMSC_ERWAM	Q46633	erwinia amy
31	33	57.9	465	1	LIPP_CAVPO	P50903	cavia porce
32	33	57.9	498	1	ACHP_HUMAN	P30926	homo sapien
33	33	57.9	603	1	NMBL_MOUSE	Q08919	mus musculu

ALIGNMENTS

RESULT 1

CTAG_HUMAN	STANDARD;	PRT;	180 AA.
ID CTAG_HUMAN			
AC P78358;			
DT 15-DEC-1998 (Rel. 37, Created)			
DT 15-DEC-1998 (Rel. 37, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE Autoimmunogenic cancer/testis antigen NY-ESO-1.			
GN CTAG.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
NCBI_TaxID=9606;			
[1]			
SEQUENCE FROM N.A.			
RX MEDLINE=97203161; PubMed=9050879;			
RA Chen Y.-T., Scanlan M.J., Sahn U., Tuereci O., Gure A.O., Tsang S., Williamson B., Stockert E., Ffreundschuh M., Old L.J.;			
RA "A testicular antigen aberrantly expressed in human cancers detected by autologous antibody screening."			
RT Proc. Natl. Acad. Sci. U.S.A. 94:1914-1918(1997).			
RL RN [2]			
SEQUENCE FROM N.A.			
RC MEDLINE=98430682; PubMed=9759882;			
RX MEDLINE=98289962; PubMed=9626360;			
RA Lethe B., Lucas S., Michaux L., de Smet C., Godelaine D., Serrano A., de Plaein E., Boon T.;			
RA "LAGE-1 a new gene with tumor specificity."			
RT Int. J. Cancer 76:903-908(1998).			
RL RN [3]			
SEQUENCE FROM N.A.			
RX MEDLINE=98430682; PubMed=9759882;			
RA Wang R.-F., Johnston S.L., Zeng G., Topalian S.L., Schwartzentruber D.J., Rosenberg S.A.;			
RA "A breast and melanoma-shared tumor antigen: T cell responses to antigenic peptides translated from different open reading frames."			
RT J. Immunol. 161:3596-3606(1998).			
CC 1- TISSUE SPECIFICITY: EXPRESSED IN TESTIS AND OVARY AND IN A WIDE VARIETY OF CANCERS. DETECTED IN UTERINE MYOMETRIUM.			
CC -! SIMILARITY: STRONG, TO LAGE-1.			
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CC EMBL; U87459; AAB49693.1; .			
CC EMBL; AJ003149; CAA05908.1; .			
CC EMBL; AF038567; AAD05202.1; .			
CC MIM; 301056; .			
KW Transmembrane; Antigen.			
CC DOMAIN 5 82			
FT TRANSMEM 156 172			

SQ	SEQUENCE	180 AA;	17992 MW;	B122C5C2C8BE1569 CRC64;	
	Query Match	100.0%;	Score 57;	DB 1;	Length 180;
	Best Local Similarity	100.0%;	Pred. No. 0.0039;		
	Matches	10;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	LLMWITQCF1 10 			
Db	158	LLMWITQCF1 167			
RESULT 2					
ID	ATP6_BUCAI	STANDARD;	PRT;	274 AA.	
AC	P57118;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DE	ATP synthase A chain (EC 3.6.3.14) (Protein 6).				
GN	ATPB OR BU002.				
OS	Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium).				
OS	Bacterium; Proteobacteria; gamma subdivision; Buchnera.				
OC	NCBI_TaxID=118099;				
OX	[1]				
RN	SEQUENCE FROM N.A.				
RC	STRAIN=TOKYO 1998;				
RX	MEDLINE=20445173; PubMed=10993077;				
RA	Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;				
RT	"Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS."				
RL	Nature 407:81-86(2000).				
CC	-!- FUNCTION: KEY COMPONENT OF THE PROTON CHANNEL; IT MAY PLAY A DIRECT ROLE IN THE TRANSLOCATION OF PROTONS ACROSS THE MEMBRANE (BY SIMILARITY).				
CC	-!- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).				
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).				
CC	-!- SIMILARITY: BELONGS TO THE ATPASE A CHAIN FAMILY.				
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CC	EMBL; AP001118; BAB12730.1; InterPro; IPR000568; ATP_synt_A; Pfam; PF00119; ATP-synt_A; PR00123; ATPSEA.				
DR	PROSITE; PS00449; ATPASE_A; 1.				
KW	Hydrogen ion transport; CF(0); Transmembrane; Complete proteome.				
FT	TRANSMEM 44 64. POTENTIAL.				
FT	TRANSMEM 110 130 POTENTIAL.				
FT	TRANSMEM 156 176 POTENTIAL.				
FT	TRANSMEM 179 199 POTENTIAL.				
FT	TRANSMEM 212 232 POTENTIAL.				
FT	TRANSMEM 243 263 POTENTIAL.				
SQ	SEQUENCE 274 AA; 31363 MW; 4B2321336EFE78A4 CRC64;				
Query Match 75.48;					
	Best Local Similarity 80.0%;	Pred. No. 1.4;	Score 43;	DB 1;	Length 274;
	Matches 8;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1	LLMWITQCF1 10 			
Db	229 LLPWWTQCF1 238				
RESULT 3					
YQIA_ECOLI	STANDARD;				
ID	YQIA_ECOLI				
AC	P36653;				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
Query Match 64.98;					
	Best Local Similarity 55.6%;	Pred. No. 20;	Score 37;	DB 1;	Length 365;
	Matches 5;	Conservative 3;	Mismatches 1;	Indels 0;	Gaps 0;
QY	2	LMWITQCF1 10 : : :			
Db	117 LLWLROCW1 125				
RESULT 4					
YQIA_ECOLI	STANDARD;				
ID	YQIA_ECOLI				
AC	P36653;				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				

KW Hydrolase; Hydrogen ion transport.
 SQ SEQUENCE 351 AA; 40791 MW; 5E1A67A149AC4EF4 CRC64;

Query Match 63.2%; Score 36; DB 1; Length 351;
 Best Local Similarity 71.4%; Pred. No. 29;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LMWITQC 8
 Db 328 LMWSEC 334

RESULT 6
 V0D2_ARATH STANDARD; PRT; 351 AA.

ID Q9LHA4;
 AC DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Probable vacuolar ATP synthase subunit d 2 (EC 3.6.3.14) (V-ATPase d subunit 2) (vacuolar proton pump d subunit 2).
 GN AT3G28715 OR MZN14_22.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis; Arabidopsis II;
 OC NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M., Furtmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.; Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P., RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P., Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V., Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S., Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G., Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simionati B., Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G., Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J., Navarro P., Collado C., Perez-Pereira A., Ottenwaelder B., Duchemin D., Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D., RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E., Monfort A., Argiriou A., Flores M., Liquori R., Vitale D., RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W., Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J., Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P., Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., van Aken S., RA Pai G., Millitscher J., Sellers P., Gill J.E., Feldblum T.V., Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C., Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E., Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y., RA Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Muraki A., Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis thaliana.";
 RT Nature 408:820-822(2000).
 CC -!- FUNCTION: SUBUNIT OF THE INTEGRAL MEMBRANE V0 COMPLEX OF VACUOLAR ATPASE. VACUOLAR ATPASE IS RESPONSIBLE FOR ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS, THUS PROVIDING MOST OF THE ENERGY REQUIRED FOR TRANSPORT PROCESSES IN THE VACUOLAR SYSTEM.
 CC -!- SUBUNIT: V-ATPase is an heteromultimeric enzyme composed of a peripheral catalytic V1 complex (components A to H) attached to an integral membrane V0 proton pore complex (components: a, c, c', c'', and d).
 CC -!- SIMILARITY: BELONGS TO THE V-ATPASE V0D/AC39 SUBUNIT FAMILY.

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DR EMBL; AP002057; BAB03168.1;
 DR EMBL; AP000420; BAB03168.1; JOINED.
 DR InterPro; IPR002843; VATP-synt_AC39.
 DR Pfam; PF01992; VATP-synt_AC39; 1.
 KW Hydrolase; Hydrogen ion transport.
 SQ SEQUENCE 351 AA; 40787 MW; DEA55CA48329E544 CRC64;

RESULT 7
 TPS3_YEAST STANDARD; PRT; 1022 AA.

ID TPS3_YEAST
 AC P38426;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Alpha, alpha-trehalose-phosphate synthase [UDP-forming] 115 kDa subunit (EC 2.4.1.15) (Trehalose-6-phosphate synthase) (UDP-glucose-glycosidase glucosyltransferase).
 GN TPS3 OR YMR261C OR YM8156_03C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomyces; Saccharomyces.
 OC Saccharomycetales; Saccharomyctaceae; Saccharomyces.
 NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Manning A.M., Rosenblom C.L., Beaudet A.L.;
 RL Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Lye G., Churcher C.M., Barrell B.G., Rajandream M.A.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
 CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-glucose 6-phosphate + alpha,alpha-trehalose 6-phosphate.
 CC -!- SUBUNIT: TREHALOSE SYNTHASE/PHOSPHATASE COMPLEX CONTAINS THREE OR FOUR POLYPEPTIDES OF 56 kDa (TPS1), 102 kDa (TPS2), 115 kDa (TPS3) AND 123 kDa (TSL1).
 CC -!- INDUCTION: REPRESSSED BY GLUCOSE.
 CC -!- SIMILARITY: CONTAINS A DOMAIN FOUND IN ALL THE PROTEINS OF THE TPS COMPLEX.
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DR EMBL; M88172; AAA35224.1; ALT_INIT.
 DR EMBL; Z49260; CAA89244.1; ALT_INIT.
 DR SGD; S0004874; TPS3.
 DR InterPro; IPR001830; Glyco_transf_20.
 DR InterPro; IPR003337; Trehalose_PPhase.
 DR Pfam; PF00982; Glyco_transf_20; 1.
 DR Pfam; PF02358; Trehalose_PPhase; 1.
 KW Transferase; Glycosyltransferase; Glycolysis.

RA Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,

RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae."

RT Nucleic Acids Res. 24:4420-4449(1996).-
RL STRONG, TO M.GENITALIUM MG060.

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DR EMBL; AE000010; AAB95728.1; -.
DR InterPro; IPR001173; Glycos_transf_2.

DR PF00535; Glycos_transf_2; 1.

KW Hypothetical protein; Transferase; Glycosyltransferase;

KW Complete proteome.

SEQUENCE 299 AA; 35079 MW; 6E3F89EDAE420417 CRC64;

Query Match 61.4%; Score 35; DB 1; Length 299;
Best Local Similarity 71.4%; Pred. No. 37;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 WITQCF1 10
Db 274 WYTRCFL 280

RESULT 11
FCG2_CAVPO STANDARD; PRT; 341 AA.
ID Q60513; Q60512; Q60511; Q60498;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Low affinity immunoglobulin gamma FC region receptor II precursor (FC-gamma RII) (FCRII) (IGG FC receptor II) (FC-gamma-1/gamma-2 receptor).
DE FCGR2.
GN Cavia porcellus (Guinea pig)
OS Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
NCBI_TaxID=10141;

[1]

RN RP SEQUENCE FROM N.A. (ISOFORM 2R-B1).
RX MEDLINE=90241239; PubMed=8345193;

RA Yamashita T., Shinohara K., Yamashita Y.;
RT "Expression cloning of complementary DNA encoding three distinct isoforms of guinea pig FC receptor for IgG1 and IgG2.";
RL J. Immunol. 151:2014-2023(1993).

CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS GAMMA. LOW AFFINITY RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 2R-B1, 2R-B2 AND 2R-B3 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -!- TISSUE SPECIFICITY: MACROPHAGES AND POLYMORPHONUCLEAR LEUKOCYTES EXPRESS PREFERENTIALLY 2R-B1. B LYMPHOCYTES EXPRESS ALL THREE FORMS.

CC -!- DOMAIN: CONTAINS AN INTRACYTOPLASMIC MOTIF REFERRED AS IMUNORECEPTOR TYROSINE-BASED INHIBITOR MOTIF (ITIM). THIS MOTIF IS INVOLVED IN DOWNMODULATION OF CELLULAR FUNCTIONS.

CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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CC EMBL; D13693; BAA02852.1; -.
CC EMBL; D13692; BAA02851.1; -.
CC EMBL; D13691; BAA02850.1; -.
CC HSSP; P12319; 1ALT.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003600; Ig_like.
CC Pfam; PF00047; iq; 2.
CC SMART; SM00409; Ig; 1.
CC SMART; SM00410; Ig_like; 1.
CC IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal; Potential; Alternative splicing.

CC LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION RECEPTOR II.
KW Immunoglobulin domain; Repeat; Immunoglobulin domain; Repeat; Potential.
FT SIGNAL 1 42
FT CHAIN 43 341
FT DOMAIN 4 3
FT TRANSMEM 225 245
FT DOMAIN 246 341
FT DOMAIN 64 120
FT DOMAIN 145 203
FT DOMAIN 318 323
FT DISULFID 71 113
FT DISULFID 152 196
FT CARBOHYD 79 79
FT CARBOHYD 106 106
FT CARBOHYD 180 180
FT CARBOHYD 187 187
FT CARBOHYD 195 195
FT VARSPLITC 273 301
FT VARSPLIC 257 301
FT CONFLICT 114 114
SQ SEQUENCE 341 AA; 37091 MW; 5137E3271D443B84 CRC64;

Query Match 61.4%; Score 35; DB 1; Length 341;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 28 MLJWITVLFL 37

RESULT 12
UBR1_YEAST STANDARD; PRT; 1950 AA.
ID UBR1_YEAST P19812;
AC P19812;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE N-end-recognizing protein (Ubiquitin-protein ligase E3 component) (N-recognin).
GN UBR1 OR PTR1 OR YGR184C OR G7168;
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyces;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2R-B1).
RN 5137E3271D443B84 CRC64;

RC STRAIN=S288C / GRF88;
 RX MEDLINE=91006011; PubMed=2209542;
 RA Bartel B., Wuennen I., Varschavsky A.;
 RT "The recognition component of the N-end rule pathway.";
 RL EMBO J. 9:3179-3189(1990).
 [2]
 RN SEQUENCE FROM N.A.
 RP Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECOGNITION COMPONENT OF THE N-END RULE PATHWAY. BINDS
 TO PROTEINS BEARING AMINO-TERMINAL RESIDUES THAT ARE DESTABILIZING
 ACCORDING TO THE N-END RULE, BUT DOES NOT BIND TO OTHERWISE
 IDENTICAL PROTEINS BEARING STABILIZING AMINO-TERMINAL RESIDUES.
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 CC
 DR X53747; CAA37779.1; ..
 DR X99074; CAA67528.1; ..
 DR EMBL; Z72969; CAA97210.1; ..
 DR PIR; S12332; S12332.
 DR SGD; S0003416; UBR1.
 DR InterPro; IPR003126; Znf_UBR1.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF02207; zf-UBR1; 1.
 DR SMART; SM00184; RING; 1.
 DR SMART; SM00396; Znf_UBR1; 1.
 DR Ligase; Ubiquitin conjugation.
 SEQUENCE 1950 AA; 224836 MW; 33E4CD3A031AF523 CRC64;
 KW Ligase; Ubiquitin conjugation.
 SQ SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85137888; PubMed=3871915;
 RA Kranz D.M., Saito H., Heller M., Takagaki Y., Haas W., Eisen H.N.,
 RA Tonegawa S.;
 RT "Limited diversity of the rearranged T-cell gamma gene.";
 RL Nature 313:752-755(1985).
 DR PIR; A02019; RWMS12.
 DR HSSP; P01709; 2MCG.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; Igv; 1.
 DR T-cell; Receptor; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 132
 T-CELL RECEPTOR GAMMA CHAIN V REGION
 DFL12.
 FT DOMAIN 19 114
 FT DOMAIN 115 132
 J SEGMENT.
 FT NON_TER 132 132
 SQ SEQUENCE 132 AA; 15434 MW; 855D714D04A3CCFE CRC64;
 L.
 Query Match 61.4%; Score 35; DB 1; Length 1950;
 Best Local Similarity 50.0%; Pred. No. 2.1e+02;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LLMWITQC 8
 Db 395 IILWITHC 402
 RESULT 13
 RRPL_UUK
 ID RRPL_UUK
 STANDARD; PRT; 2103 AA.
 AC P33453;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RNA-directed RNA polymerase (EC 2.7.7.48) (L protein).
 GN Uukuniemi virus (Uuk).
 OS Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
 OC NCBI_TaxID=11591;
 OX [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=S23;
 RX MEDLINE=92333259; PubMed=1629699;
 RA Elliott R.M., Dunn E., Simons J.F., Pettersson R.F.;
 RT "Nucleotide sequence and coding strategy of the Uukuniemi virus L RNA
 segment.";

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ID TVC1_MOUSE STANDARD; PRT; 135 AA.
AC P01740;
DT 21-JUL-1986 (Rel. 01, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE T-cell receptor gamma chain V region V108A precursor.
OS Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=85099339; PubMed=3917858;
RA Hayday A.C., Saito H., Gillies S.D., Kranz D.M., Tanigawa G.,
RA Eisen H.N., Tonegawa S. ;
RT "Structure, organization, and somatic rearrangement of T cell gamma
genes." ;
RL Cell 40:259-269 (1985).
RN [2]
RP SEQUENCE FROM N.A. (CLONE PHDS4/PHDS203).
RC STRAIN=BALB.B;
RX MEDLINE=84245824; PubMed=6330561;
RA Saito H., Kranz D.M., Takagaki Y., Hayday A.C., Eisen H.N.,
RA Tonegawa S. ;
RT "Complete primary structure of a heterodimeric T-cell receptor
deduced from cDNA sequences." ;
RL Nature 309:757-762 (1984).
CC -!- MISCELLANEOUS: THIS mRNA WAS ISOLATED FROM A CYTOTOXIC
CC T-LYMPHOCYTE. THE GENE CORRESPONDING TO THIS mRNA IS REARRANGED
CC SPECIFICALLY IN T CELLS AND ITS ORGANIZATION IS SIMILAR TO AN Ig
CC GENE, WITH V (OR V+D), J, AND C REGIONS.
DR PIR; A02018; RWMSV1.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR T-cell; Receptor; Signal.
KW SIGNAL
FT SIGNAL 1 18
FT CHAIN 19 135 T-CELL RECEPTOR GAMMA CHAIN V REGION
FT V108A.
FT DOMAIN 19 116 V SEGMENT.
FT DOMAIN 117 135 J SEGMENT.
FT NON_TER 135 135
SQ SEQUENCE 135 AA; 15930 MW; 402145C95E924D7D CRC64;

```

Query Match 59.6%; Score 34; DB 1; Length 135;
 Best Local Similarity 60.0%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

Qy 1 LLMWITQCFL 10
   | | | | |
   3 LLRWFTSCL 12

```

Search completed: July 16, 2002, 08:00:43
 Job time: 821 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 16, 2002, 07:45:57 ; Search time 89.54 Seconds
(without alignments)
19.320 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
Gapext 10.0 , Gapext 0.5

Searched: 5622222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 5622222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:
 1: sp_archaea:
 2: sp_bacteria:
 3: sp_fungi:
 4: sp_human:
 5: sp_invertebrate:
 6: sp_mammal:
 7: sp_mhc:
 8: sp_organelle:
 9: sp_phage:
 10: sp_plant:
 11: sp_rabbit:
 12: sp_virus:
 13: sp_vertebrate:
 14: sp_unclassified:
 15: sp_virus:
 16: sp_bacteriap:
 17: sp_archeap:

Result No.	Score	Query	Match	Length	DB	ID	Description
1	57	100.0	180	4	Q9Y479		Q9y479 homo sapien
2	44	77.2	151	4	Q9UJK3		Q9ujk3 homo sapien
3	44	77.2	593	4	Q96NH3		Q96nh3 homo sapien
4	38	66.7	65	1	Q46517		Q46517 desulfuroco
5	38	66.7	152	12	Q9PX35		Q9px35 equine arte
6	38	66.7	152	12	Q9PX34		Q9px34 equine arte
7	38	66.7	152	12	Q9QKH1		Q9qkh1 equine arte
8	38	66.7	152	12	Q9QKG6		Q9qkg6 equine arte
9	38	66.7	152	12	Q9QKF2		Q9qkf2 equine arte
10	38	66.7	273	5	Q962M9		Q962m9 plasmidium
11	38	66.7	408	16	Q9KRM7		Q9krm7 vibrio chol
12	38	66.7	423	5	Q02168		Q02168 caenorhabdi
13	38	66.7	996	10	Q9SGP2		Q9sgp2 arabidopsis
14	37.5	65.8	83	12	Q9WGD6		Q9wgd6 human papil
15	37	64.9	317	5	Q97336		Q97336 plasmidium
16	37	64.9	783	3	Q14411		Q14411 candida alb

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT	1	Q9Y479	PRELIMINARY;	PRT;	180 AA.
ID	Q9Y479;				
AC	Q9Y479;				
DT	01-NOV-1999 (TREMBLrel. 12, Created)				
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	LAGE-1S PROTEIN (CANCER/TESTIS ANTIGEN 2).				
GN	LAGE1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
NCBI_TaxID	9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=MELANOMA;				
RX	MEDLINE=9932550; PubMed=10399963;				
RA	Aarnoudse C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;				
RT	"Interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an unexpected translation product of LAGE-1.";				
RT	Int. J. Cancer 82:442-448(1999).				
RL	[2]				
RN	SEQUENCE FROM N.A.				
RA	Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,				
RA	Patlan H., Ciccodicola A., Kenwrick S., Platzer M., D'Urso M.,				
RA	Nelson D.L.;				
RT	"Multiple pathogenic and benign genomic rearrangements occur at a 35-kb duplication involving the NEMO and the LAGE2 genes."				
RT	Hum. Mol. Genet. 0:0-0(2001).				
RL	EMBL; AJ012834; CAA10194.1; -.				
DR	EMBL; AF277315; AAL27015.1; -.				
SQ	SEQUENCE 180 AA; 18236 MW; 9077FAF953543A25 CRC64;				

Query Match 100.0%; Score 57; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LLMWITQCFL 10

RESULT 6	Q9PX34; PRELIMINARY;	PRT; 152 AA.	RESULT 8	Q9QKG6; PRELIMINARY;	PRT; 152 AA.
ID Q9PX34;			ID Q9QKG6;		
AC Q9PX34;			AC Q9QKG6;		
DT 01-MAY-2000 (TREMBLrel. 13, Created)			DT 01-MAY-2000 (TREMBLrel. 13, Created)		
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE ORF4.			DE ORF4.		
OS Equine arteritis virus (EAV).			OS Equine arteritis virus (EAV).		
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;			OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;		
OC Arteriviridae; Arterivirus.			OC Arteriviridae; Arterivirus.		
OC NCBI_TaxID=11047;			OC NCBI_TaxID=11047;		
RN [1]			RN [1]		
RP SEQUENCE FROM N.A.			RP SEQUENCE FROM N.A.		
RC STRAIN=P2, A2, A3, AND A4;			RC STRAIN=R2;		
RX MEDLINE=99394666; PubMed=10466790;			RX MEDLINE=99394666; PubMed=10466790;		
RA Balasuriya U.B.R., Hedges J.F., Nadler S.A., McCollum W.H., Timoney P.J., MacLachlan N.J.;			RA Balasuriya U.B., Hedges J.F., Nadler S.A., McCollum W.H., Timoney P.J., MacLachlan N.J.;		
RT "Genetic Stability of Equine Arteritis Virus during Horizontal and Vertical Transmission in an Outbreak of Equine Viral Arteritis.";			RT "Genetic stability of equine arteritis virus during horizontal and vertical transmission in an outbreak of equine viral arteritis.";		
RL J. Gen. Virol. 80:1949-1958 (1999).			RL J. Gen. Virol. 80:1949-1958 (1999).		
DR EMBL; AF118770; AAD54689.1; .			DR EMBL; AF118774; AAD54713.1; .		
DR EMBL; AF118771; AAD54695.1; .			DR InterPro; IPR004257; GP4.		
DR EMBL; AF118772; AAD54701.1; .			DR Pfam; PF03010; GP4; 1.		
DR InterPro; IPR004257; GP4.			SQ SEQUENCE 152 AA; 17124 MW; 5F8FF3D15420985F CRC64;		
DR Pfam; PF03010; GP4; 1.			SQ SEQUENCE 152 AA; 17082 MW; CF18AEAA1B9D756B CRC64;		
SQ SEQUENCE 152 AA; 17124 MW; 5F8FF3D15420985F CRC64;					
Query Match 66.7%; Score 38; DB 12; Length 152;			Query Match 66.7%; Score 38; DB 12; Length 152;		
Best Local Similarity 50.0%; Pred. No. 17;			Best Local Similarity 50.0%; Pred. No. 17;		
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;			Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;		
QY 1 LLMWITQFL 10			QY 1 LLMWITQFL 10		
: : :			: : :		
Db 143 LVRWVQQCYL 152			Db 143 LVRWVQQCYL 152		
RESULT 7	Q9QKH1; PRELIMINARY;	PRT; 152 AA.	RESULT 9	Q9QKF2; PRELIMINARY;	PRT; 152 AA.
ID Q9QKH1;			ID Q9QKF2;		
AC Q9QKH1;			AC Q9QKF2;		
DT 01-MAY-2000 (TREMBLrel. 13, Created)			DT 01-MAY-2000 (TREMBLrel. 13, Created)		
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE ORF4.			DE ORF4.		
OS Equine arteritis virus (EAV).			OS Equine arteritis virus (EAV).		
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;			OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;		
OC Arteriviridae; Arterivirus.			OC Arteriviridae; Arterivirus.		
OC NCBI_TaxID=11047;			OC NCBI_TaxID=11047;		
RN [1]			RN [1]		
RP SEQUENCE FROM N.A.			RP SEQUENCE FROM N.A.		
RC STRAIN=AI;			RC STRAIN=RO;		
RX MEDLINE=99394666; PubMed=10466790;			RX MEDLINE=99394666; PubMed=10466790;		
RA Balasuriya U.B., Hedges J.F., Nadler S.A., McCollum W.H., Timoney P.J., MacLachlan N.J.;			RA Balasuriya U.B., Hedges J.F., Nadler S.A., McCollum W.H., Timoney P.J., MacLachlan N.J.;		
RT "Genetic stability of equine arteritis virus during horizontal and vertical transmission in an outbreak of equine viral arteritis.";			RT "Genetic stability of equine arteritis virus during horizontal and vertical transmission in an outbreak of equine viral arteritis.";		
RL J. Gen. Virol. 80:1949-1958 (1999).			RL J. Gen. Virol. 80:1949-1958 (1999).		
DR EMBL; AF118769; AAD54683.1; .			DR EMBL; AF118782; AAD54761.1; .		
DR InterPro; IPR004257; GP4.			DR InterPro; IPR004257; GP4.		
DR Pfam; PF03010; GP4; 1.			SQ SEQUENCE 152 AA; 17138 MW; 0E5AF3C417BC256F CRC64;		
SQ SEQUENCE 152 AA; 16995 MW; 5F8FE7815B70835F CRC64;			SQ SEQUENCE 152 AA; 17138 MW; 0E5AF3C417BC256F CRC64;		
Query Match 66.7%; Score 38; DB 12; Length 152;			Query Match 66.7%; Score 38; DB 12; Length 152;		
Best Local Similarity 50.0%; Pred. No. 17;			Best Local Similarity 50.0%; Pred. No. 17;		
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;			Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;		
QY 1 LLMWITQFL 10			QY 1 LLMWITQFL 10		
: : :			: : :		
Db 143 LVRWVQQCYL 152			Db 143 LVRWVQQCYL 152		

RESULT 10
 Q962M9 PRELIMINARY; PRT; 273 AA.
 ID Q962M9;
 AC Q962M9;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PV1H14025_P.
 GN T20F7_6.
 OS Plasmodium vivax.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5855;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tchavtchitch M., Fischer K., Huestis R., Saul A.;
 RT "The sequence of 200 kb portion of a Plasmodium vivax chromosome
 reveals a high degree of conservation with *P. falciparum* chromosome
 3.";
 RT MOL: Biochem. Parasitol. 0:0-0(2001).
 DR EMBL; AY003872; AAF99451.1; -.
 SQ SEQUENCE 273 AA; 32028 MW; 73F0E1666635A30C CRC64;
 [2]
 Query Match 66.7%; Score 38; DB 5; Length 273;
 Best Local Similarity 66.7%; Pred. No. 29;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 [3]
 Qy 1 LLMWITQCF 9
 | : | |||
 db 27 LLIWTLQCF 35
 [1]
 RESULT 11
 Q9KRM7 PRELIMINARY; PRT; 408 AA.
 ID Q9KRM7;
 AC Q9KRM7;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL PROTEIN VC1609.
 GN VC1609.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibionaceae; Vibrio.
 OX NCBI_TaxID=66;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 Fraser C.M.;
 RA "DNA sequence of both chromosomes of the cholera pathogen *Vibrio
 cholerae*.";
 RT Nature 406:477-483(2000).
 RL EMBL; AE004238; AAF94763.1; -.
 DR TIGR; VC1609; -.
 KW Complete proteome.
 SQ SEQUENCE 408 AA; 44619 MW; B786CB2501E37C8C CRC64;
 [1]
 RESULT 12
 Q9216B PRELIMINARY; PRT; 423 AA.
 ID 00216B;
 AC 00216B;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 47.5 KDA PROTEIN.
 GN T20F7_6.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderrinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 investigating biology. The *C. elegans* Sequencing Consortium.";
 DR Science 282:2012-2018(1998).
 RL [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Miller N., Gattung S.;
 RT "The sequence of *C. elegans* cosmid T20E7.";
 RL Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U97550; AAK18981.2; -.
 KW Hypothetical protein.
 SQ SEQUENCE 423 AA; 47451 MW; 6997065D515E7B21 CRC64;
 [1]
 Query Match 66.7%; Score 38; DB 5; Length 423;
 Best Local Similarity 62.5%; Pred. No. 44;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 LMWITQCF 9
 | : | |||:
 Db 43 LLWLNQCY 50
 [1]
 RESULT 13
 Q9SGP2 PRELIMINARY; PRT; 996 AA.
 ID Q9SGP2;
 AC Q9SGP2;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 13, Last annotation update)
 DE F3M18.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
 Kim C., Altafai H., Bei Q., Chin C., Choi E., Conn L.,
 Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
 Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 Ecker J.R.;
 RT "Genomic sequence for *Arabidopsis thaliana* BAC F3M18 from chromosome
 I.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AC010155; AAF16764.1;
DR InterPro; IPR001611; Euk_pk kinase.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR003592; Ser_thr_pk kinase.
DR InterPro; IPR002290; Ser_thr_pk kinase.
DR PF00560; LRR; 22.
DR Pfam; PF00069; kinase; 1.
DR PRINTS; PRO0019; LEURICHRPT.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00370; LRR; 18.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SEQUENCE 996 AA; 108929 MW; 9C9A6A708A1F933A CRC64;

Query Match 66.7%; Score 38; DB 10; Length 996;
Best Local Similarity 55.6%; Pred. No. 97; Gaps 0;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 LMWITQCFL 10
:||:||:|| 1
Db 209 VMNLTECHL 217

RESULT 14
Q9WGDD6 PRELIMINARY; PRT; 83 AA.
ID Q9WGDD6
AC 09WGDD6;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE E5 PROTEIN.
GN E5.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TAXID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IS808;
RX MEDLINE=99190418; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments."
RT J. Virol. 69:7743-7753(1995).
RL [2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=IS808;
RX MEDLINE=99190418; PubMed=10091997;
RA Eriksson A., Herron J.R., Yamada T., Wheeler C.M.;
RT "Human papillomavirus type 16 variant lineages characterized by
nucleotide sequence analysis of the E5 coding segment and the E2 hinge
region."
RT J. Gen. Virol. 80:595-600(1999).
DR EMBL; AF120707; AAD24035.1;
DR InterPro; IPR004270; Papilloma_E5.
DR Pfam; PF03025; Papilloma_E5; 1.
SQ SEQUENCE 83 AA; 9387 MW; B57D5DD3DD77CB7E CRC64;

Query Match 65.8%; Score 37.5; DB 12; Length 83;
Best Local Similarity 53.3%; Pred. No. 12;
Matches 8; Conservative 2; Mismatches 0; Indels 5; Gaps 1;
QY 1 LMWIT----QCFL 10
:||:||:|| 1
Db 47 LMWITAAASAFRCFL 61

RESULT 15
O97336 PRELIMINARY;
ID O97336; PRT; 317 AA.
AC 097336;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PFC0085C, MAL3P8.15 PROTEIN.
GN PFC0085C, MAL3P8.15.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TAXID=36329;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=99376085; PubMed=10448855;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltwell T.,
RA Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagels K., Jassal B., McLean J., Moule S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Rutter S., Skelton J., Squares S., Sulston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
RT "The complete nucleotide sequence of chromosome 3 of Plasmodium
falciparum";
RL Nature 400:532-538(1999).
DR EMBL; AL034560; CAB39133.2;
SQ SEQUENCE 317 AA; 37389 MW; 26CF0DC38C651474 CRC64;

Query Match 64.9%; Score 37; DB 5; Length 317;
Best Local Similarity 55.6%; Pred. No. 51;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 LMWITQCFL 9
Db 51 IFIWICQCF 59

Search completed: July 16, 2002, 07:59:50
Job time: 833 sec

PT Cancer antigen NY ESO1/CAG-3
 XX Example 10; Page 42; 88pp; English.
 CC This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified. The present peptide (ranked 16) corresponds to amino acid residues 158-167 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, bladder cancer, cervical cancer, cervical cancer, kidney cancer, prostate, ovarian, pancreatic and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers.

XX Sequence 10 AA;

Query Match 2
 Best Local Similarity 100.0%; Score 57; DB 20; Length 10;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLMWITQCFL 10
 Db 1 llmwitqcf1 10

RESULT 2
 ID AAY52434 standard; peptide; 10 AA.
 XX AAY52434;
 XX DT 15-FEB-2000 (first entry)

DE Human tumour antigen NY-ESO-1 peptide #7.
 XX Cancer; tumour; antigen; MHC; major histocompatibility complex; Class I;
 KW T-cell; cytotoxic; stimulation; proliferation; treatment;
 KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
 KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
 KW lymphoma.

XX Synthetic.
 OS Homo sapiens.
 XX PN WO9953938-A1.
 XX PD 28-OCT-1999.
 XX PF 24-MAR-1999; 99WO-US06875.
 XX PR 17-APR-1998; 98US-0062422.
 XX PR 02-OCT-1998; 98US-0165546.
 XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
 PI Gure A, Ritter G;
 XX DR WPI; 2000-038483/03.

XX Novel peptides which bind to MHC class I and MHC class II molecules, useful for therapeutic and diagnostic purposes -
 XX Claim 55; Page 20; 49pp; English.

CC Peptides #4-#7 (AAY52431-Y52434) are peptides derived from the human tumour antigen, NY-ESO-1 (AAY52430) which contain the motif LLMWIT (AAV52441). These sequences can bind to MHC (major histocompatibility Class I HLA-A2 molecules, thereby stimulating proliferation of cytotoxic T-cells. cDNA encoding NY-ESO-1 was initially isolated from an oesophagus squamous cell cancer cDNA library. Tissue localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain tumours and tumour cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens, with expression in other tumour types being sporadic. These NY-ESO-1-derived peptides may be used in methods and compositions used for the treatment, diagnosis and prevention of cancers (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to stimulate the proliferation of T cells.

XX SQ Sequence 10 AA;

Query Match 3
 Best Local Similarity 100.0%; Score 57; DB 21; Length 10;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
 Db 1 llmwitqcf1 10
 RESULT 3
 ANW622585
 ID AAW622585 standard; peptide; 11 AA.
 XX AC AAW622585;
 XX DT 17-SEP-1998 (first entry)
 XX DE Cancer associated antigen peptide.
 XX KW Cancer associated antigen; NY-ESO-1; regression; progression; onset; cancer; treatment; diagnosis.
 XX KW Synthetic.
 OS Homo sapiens.

XX PN WO9814464-A1.
 XX PD 09-APR-1998.
 XX PF 15-SEP-1997; 97WO-US163335.
 XX PR 03-OCT-1996; 96US-0725182.
 XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Chen Y, Drijfhout JW, Gure A, Jager E, Knuth A;
 PI Old LJ, Scanlan M;
 XX DR WPI; 1998-286417/25.
 XX PT New isolated cancer associated antigen - is used to develop products for the diagnosis and treatment of cancers and for monitoring cancer therapy

XX PS Claim 33; Page 17; 49pp; English.

XX Peptides AAW622585-87 are derived from cancer associated antigen NY-ESO-1, and are stimulators of cytotoxic T-cells. The specification describes a method for determining regression, progression of onset of a cancerous condition, comprising monitoring a sample from a patient with the cancerous condition for a parameter selected from NY-ESO-1 protein, a peptide derived from NY-ESO-1 protein and cytolytic

CC T cells specific for the peptide and an MHC molecule with which it
 CC non-covalently complexes. Methods for the treatment of a cancerous
 CC condition are also described. The NY-ESO-1 protein and peptides derived
 CC from it can be used for diagnosis and treatment of cancers and to
 CC monitor the efficacy of a therapeutic regime.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 19; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF1 10
 Db 2 llmwitqcf1 11

RESULT 4

AY01761

ID AY01761 standard; Peptide; 11 AA.

XX AC AY01761;

XX DT 25-JUN-1999 (first entry)

DE Exemplary antigenic peptide derived from NY-ESO-1.

XX KW MAGE-3; tumour associated gene; human leucocyte antigen Class II;
 XX autologous CD4+ cell; MAGE-3 related disease; cancer; melanoma;
 XX osteosarcoma; leukemia; carcinoma.

XX OS Homo sapiens.

XX PN WO9914326-A1.

XX PD 25-MAR-1999.

XX PF 04-SEP-1998; 98WO-US18601.

XX PR 12-SEP-1997; 97US-0928615.

XX PA (LUDW-) LUDWIG INST CANCER RES.

PA (UYVR-) UNIV VRIJE BRUSSEL.

PI Boon-Falleur T, Chaux P, Corthals J,

PI Heirman C;

PI Luiten R, Stroobant V, Thielemans K,

PI Van Der Bruggen P;

XX DR 1999-244031/20.

Isolated peptides that bind to human leucocyte antigen class II
 PT molecules

XX Disclosure; Page 29; 88pp; English.

XX PS

XX The present sequence represents an exemplary tumour associated peptide

CC antigen. The specification describes a MAGE-3 tumour associated gene.

Peptides (AY01721-25) that bind human leucocyte antigen (HLA) Class II
 CC molecules can be derived from the MAGE-3 protein. These peptides and
 CC autologous CD4+ cells that bind to a complex of MAGE-3 peptide
 CC and HLA Class II, are used to treat MAGE-3 related diseases,
 CC particularly cancers (e.g. melanoma, osteosarcoma, leukemia and
 CC various forms of carcinoma). The peptides are also used to produce
 CC specific antibodies. Detection of the peptides, e.g. in binding
 CC assays, particularly with antibodies, is used for diagnosis of such
 CC diseases.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 11 AA;

RESULT 5

AAB08702

ID AAB08702 standard; Peptide; 11 AA.

XX AC AAB08702;

XX DT 02-JAN-2001 (first entry)

XX DE Antigenic peptide from tumour rejection antigen NY-ESO-1.

XX KW EphA3; HLA Class II-binding peptide; human leukocyte antigen; antigen;

KW CD4+ T lymphocyte; tumour associated gene; vaccine.

XX OS Homo sapiens.

XX PN WO200050589-A1.

XX PD 31-AUG-2000.

XX PF 18-FEB-2000; 2000WO-US04326.

XX PR 22-FEB-1999; 99US-0121170.

XX PR 08-OCT-1999; 99US-0158566.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Chiari R, Coulie P, Boon-Falleur T;

XX DR WPI; 2000-572089/53.

XX PS Disclosure; Page 35; 107pp; English.

XX CC AAB08668-B08704 represent antigenic peptides characteristic of tumours.

CC The peptides may be combined in vaccines with a human EphA3

CC HLA (human leukocyte antigen) class II-binding peptide. EphA3 antigens, when

CC presented by an antigen presenting cell having a HLA class II molecule,

CC effectively induce activation and proliferation of CD4+ T lymphocytes.

CC EphA3 is a tumour associated gene. EphA3 HLA binding peptides are used

CC for selectively enriching a population of T lymphocytes. The peptides

CC are also used for diagnosing a disorder characterized by EphA3 or EphA3

CC HLA binding peptide expression. The peptides are also used to treat a

CC disorder characterized by EphA3 expression. The EphA3 binding peptides

CC are useful in producing vaccines and antibody.

XX SQ Sequence 11 AA;

XX Query Match 100.0%; Score 57; DB 21; Length 11;

Best Local Similarity 100.0%; Pred. No. 0.0022;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF1 10

Db 2 llmwitqcf1 11

RESULT 6

AAB22790

ID AAB22790 standard; peptide; 11 AA.

XX AC AAB22790;

XX

DT	22-DEC-2000	(first entry)
XX	NY - ESO-1 peptide epitope, SEQ ID NO:1.	J
KW	NY-ESO-1; epitope; CTL response; cytotoxic T lymphocyte; vaccine;	
KW	immunogenic; adjuvant coadministration; microbial infection;	
KW	tuberculosis; HIV; hepatitis B virus; hepatitis C virus; cancer.	
XX	Unidentified.	
OS		
XX	WO200048630-A1.	
PN		
XX	PD 24 -AUG-2000.	
XX	PF 17 -FEB-2000; 2000WO-AU00110.	
PR	17 -FEB-1999; 99AU-0008735.	
PR	27 -JUL-1999; 99AU-0001861.	
XX	PA (CSLC-) CSL LTD.	
PI	Cox JC, Drane DP;	
XX	WPI; 2000-571930/53.	
PT	Immunogenic complexes comprising negatively charged organic carriers	
PT	adjuvants and positively charged antigens for use as vaccines against	
PT	microbial infection and cancer -	
XX	Example 4; Fig 5a; 111PP; English.	
XX	The invention relates to a novel immunogenic complex comprising a charged organic carrier and a charged antigen which are electrostatically associated. The complex induces a cytotoxic T lymphocyte (CTL) response. The complex and/or vaccine can be used to treat a disease in a mammal, where the complex/vaccine elicits, in or otherwise facilitates an immune response which inhibits, halts, or prevents the onset or progression of the disease condition. In particular, the disease is a condition resulting from a microbial infection or cancer. Microbial infections which may be treated using immunogenic complex include human immunodeficiency virus (HIV), hepatitis B, hepatitis C, tuberculosis or a parasitic condition, and cancers may be treated include melanoma, prostate cancer or breast cancer complexes and vaccines simultaneously co-deliver antigen and adjuvant the same antigen presenting cell, which is often essential for induction of appropriate immune responses. Sequences AB22790-B22791 represent peptide epitopes of the positively charged protein NY-ESO-1 used exemplification of the invention.	
XX	Sequence 11 AA;	
SQ		
Query	1 LLMWITQCFL	100.0%; Score 57; DB 21; Length 11;
		Best Local Similarity 100.0%; Pred. No. 0.0022;
	2 11mwitqcfl	Matches 10; Conservative 0; Mismatches 0; Indels 0; Gap 0;
Db		
RESULT	7	
AAB02630		
ID	AAB02630 standard; Peptide; 11 AA.	
XX		
AC		
XX		
DT	18 -AUG-2000 (first entry)	
XX		
DE	Tumour associated peptide antigen from NY-ESO-1 #1.	
XX		
KW	MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;	
KW	cancer; human; tumour; tumour associated gene product.	

XX PF 25-JUN-1999; 99WO-US14493.
 XX PR 26-JUN-1998; 98US-0105839.
 XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX PI Tureci O, Sahin U, Pfreundschuh M, Rammensee G, Stevanovic S;
 PI Chen Y, Gure A, Old LJ;
 XX DR WPI; 2000-170933/15.

PT Determining the possible presence of breast, endometrial, colorectal,
 PT lung, bladder or head-neck cancer -
 PS Example 12; Page 21; 40pp; English.

XX A method has been developed for determining the possible presence of a
 CC cancer, which is not melanoma or synovial sarcoma. The method comprises
 CC assaying a sample taken from the subject to determine the expression of
 CC an SSX gene, and determining the expression as a determination of the
 CC possible presence of cancer. Expression of SSX1 gene indicates possible
 CC presence of breast, endometrial, colorectal, lung, bladder or head-neck
 CC cancer. These cancers are also detected by SSX2 and SSX4 gene
 CC expression. SSX2 gene expression additionally indicates possible presence
 CC of lymphoma, renal cell cancer, glioma and prostate cancer. Expression
 CC of SSX4 gene also indicates possible presence of ovarian or stomach
 CC cancer. SSX5 gene expression indicates the same cancers as SSX1, except
 CC breast cancer. Determining expression of SSX gene can be used to monitor
 CC progress of melanoma or synovial sarcoma, which is not cancer. The
 CC SSX-derived peptide complex stimulates proliferation of cytolytic T
 CC cells. This is useful for treating cancer, especially melanoma. AAY78464
 CC to AAY78468 represent specifically claimed HLA binding peptides for use
 CC in the method of the invention. AAZ88452 to AAZ88465 represent PCR
 CC primers used in the isolation of SSX genes in the exemplification of the
 CC present invention. AAY78469 to AAY78500, and AAY79684 to AAY79762
 CC represent peptides derived from SSX proteins or NY-ESO-1, which are used
 CC in the exemplification of the present invention.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 21; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
 DB 2 1lmwitqcf1 11

RESULT 10
 AAG67165
 ID AAG67165 standard; peptide; 11 AA.
 XX AC AAG67165;
 XX DT 13-NOV-2001 (first entry)
 XX DE Cancer testis tumour antigen NY-ESO-1 derived CTL-stimulating peptide.
 KW Cancer; tumour; antigen; MHC; major histocompatibility complex; Class I;
 KW T-cell; cytotoxic; stimulation; proliferation; treatment;
 KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
 KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
 KW lymphoma.
 OS Synthetic.
 OS Homo sapiens.
 XX PN WO9953938-A1.
 XX PD 28-OCT-1999.

XX PF 24-MAR-1999; 99WO-US06875.
 XX PR 17-APR-1998; 98US-0062422.
 XX PR 02-OCT-1998; 98US-0165546.
 XX PA (LUDW-) LUDWIG INST CANCER RES.
 XX PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
 PI Gure A, Ritter G;
 XX DR WPI; 2000-038483/03.

XX Novel peptides which bind to MHC class I and MHC class II molecules,
 PT useful for therapeutic and diagnostic purposes -
 XX PS Claim 60; Page 18; 49pp; English.

XX Peptides #4-#7 (AY52431-Y52434) are peptides derived from the human
 CC tumour antigen, NY-ESO-1 (AY52430) which contain the motif LLMWIT
 CC (AY52441). These sequences can bind to MHC (major histocompatibility
 CC Class I HLA-A2 molecules, thereby stimulating proliferation of
 CC cytotoxic T-cells. cDNA encoding NY-ESO-1 was initially isolated
 CC from an oesophagus squamous cell cancer cDNA library. Tissue
 CC localisation studies revealed it to be expressed at high levels
 CC in normal ovary and testis but not in normal colon, kidney, liver,
 CC brain, oesophagus and skin. It was expressed in certain tumours and
 CC tumour cell lines with some degree of frequency - these included
 CC melanoma specimens and cell lines, and breast and bladder cancer
 CC specimens, with expression in other tumour types being sporadic.
 CC These NY-ESO-1-derived peptides may be used in methods and
 CC compositions used for the treatment, diagnosis and prevention of
 CC cancers (such as melanoma, breast cancer, prostate cancer, lung
 CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
 CC or lymphoma) and to stimulate the proliferation of T cells.

XX SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 21; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
 DB 2 1lmwitqcf1 11

RESULT 10
 AAG67165
 ID AAG67165 standard; peptide; 11 AA.
 XX AC AAG67165;
 XX DT 13-NOV-2001 (first entry)
 XX DE Cancer testis tumour antigen NY-ESO-1 derived CTL-stimulating peptide.
 KW Cancer tumour antigen NY-ESO-1 peptide #4.
 DE Human tumour antigen NY-ESO-1 peptide #4.
 XX AC AAY52431;
 XX DT 15-FEB-2000 (first entry)
 XX Human tumour antigen NY-ESO-1 peptide; 11 AA.
 KW Cancer; tumour; antigen; MHC; major histocompatibility complex; Class I;
 KW T-cell; cytotoxic; stimulation; proliferation; treatment;
 KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
 KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
 KW lymphoma.
 OS Synthetic.
 OS Homo sapiens.
 XX PN WO9953938-A1.
 XX PD 28-OCT-1999.

XX Lethe B, Boon-Falleur T;
 PI WPI; 2001-550091/61.
 XX Genomic sequences of tumour associated antigen NY-ESO-1 (LAGE-2) useful
 PT for diagnosing testicular tumours -
 PT
 XX Example 12; Page 24; 50pp; English.
 XX The present sequence represents a peptide which is derived from cancer
 CC testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptide
 CC stimulates cytolytic T cell lines (CTLs). NY-ESO-1 is a molecule that
 CC is processed to at least one human leucocyte antigen (HLA) binding
 CC peptide, which binds to Class I and Class II major histocompatibility
 CC complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis,
 CC but not normal colon, kidney, liver or brain tissue. The presence or
 CC level of expression of NY-ESO-1 may be assayed for the diagnosis of
 CC cancer, especially testis tumours.

XX Sequence 11 AA;
 SQ Query Match 100.0%; Score 57; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
 Db 2 1lmwitqcfl 11

RESULT 11
 AAE07777
 ID AAE07777 standard; peptide; 11 AA.
 XX AC AAE07777;
 DT 06-NOV-2001 (first entry)

XX Human wildtype NY ESO-1 peptide, ESOP157-167.
 DE Human; major histocompatibility complex; MHC; vaccine; metastasis;
 XX class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
 KW immunotherapy.
 XX Homo sapiens.
 XX WO200155393-A2.
 PN 02-AUG-2001.
 PD 26-JAN-2001; 2001WO-US02765.

XX PR 28-JAN-2000; 2000US-0179004.
 PR 29-SEP-2000; 2000US-0237107.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Wang R, Rosenberg SA, Zeng G;
 XX DR WPI; 2001-496851/54.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis -
 XX Example 14; Page 62; 134pp; English.
 PS The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC

CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any
 CC given target antigen and/or hapten and to induce tumour-specific
 CC humoral-mediated immunity against cancer. The present sequence is human
 CC wildtype NY ESO-1 peptide, ESOP157-167.
 XX Sequence 11 AA;
 SQ Query Match 100.0%; Score 57; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
 Db 2 1lmwitqcfl 11

RESULT 12
 AAE06849
 ID AAE06849 standard; peptide; 11 AA.
 XX AC AAE06849;
 DT 16-OCT-2001 (first entry)
 XX DE Human NY-ESO-1 antigenic peptide #1.
 XX AC AAE06849;
 DT 16-OCT-2001 (first entry)
 XX DE Human NY-ESO-1 antigenic peptide #1.
 XX KW MAGE antigenic peptide; Human leukocyte antigen; HLA-B35; HLA-B44;
 KW tumour cell; immunostimulant; antigen presentation; cancer; melanoma;
 KW CD8+ cytotoxic T lymphocyte; colorectal; prostate; gastric carcinoma;
 KW myeloma; brain tumour; sarcoma; seminoma; ovarian tumour; cytostatic;
 KW gene therapy; tumour rejection antigen; TRA; human; NY-ESO-1;
 KW MHC; major histocompatibility complex.
 XX OS Homo sapiens.
 XX PN WO200153833-A1.
 XX PD 26-JUL-2001.
 XX PF 19-JAN-2001; 2001WO-US02008.
 XX PR 20-JAN-2000; 2000US-0177242.
 XX PR 25-OCT-2000; 2000US-0243212.
 XX PA (LUDW-) LUDWIG INST CANCER RESS.
 XX PI Luiten R, Boon-Falleur T, Van Der Bruggen P, Stroobant V;
 XX PI Demotte N, Schultz E;
 XX DR WPI; 2001-488724/53.
 XX PT Functional variants and isolated mimetics of a MAGE-A1 HLA-B35 or
 PT HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, used
 PT in diagnosis and treatment of a disorder characterized by expression of
 PT MAGE-A1 or -A3 -
 XX PS Disclosure; Page 28; 103pp; English.

XX The invention relates to functional variants and isolated mimetics of a
 CC MAGE-A1 human leucocyte antigen (HLA)-B35 or HLA-B44 binding peptide,
 CC or of a MAGE-A3 HLA-B35 binding peptide, identified by methods described
 CC

in the specification. MAGE genes encode tumour rejection antigens (TRAs) presented to T lymphocytes by HLA-B35 and HLA-B44 molecules. The MAGE antigenic peptide acts by binding to HLA molecules on tumour cells and stimulating recognition of these cells and thus signalling them to the immune system for destruction. The peptide presented by HLA molecule induces the activation and stimulation of CD8+ cytotoxic T lymphocytes. The MAGE antigenic peptide is used to treat and diagnose disorders characterised by expression of MAGE-A1 or -A3. Disorders include cancers e.g melanomas, oesophageal, lung, head and neck, breast, colorectal, prostate, renal, bladder, hepatocellular, papillary thyroid and gastric carcinomas, myelomas, brain tumours, sarcomas, seminomas, and ovarian tumours. The present sequence is human NY-ESO-1 tumour associated antigenic peptide presented by major histocompatibility complex (MHC) HLA-A2. The antigenic peptide is used in combination with peptides of the invention for inducing an immune response.

molecule on its surface, by contacting a sample containing the cell with the peptide or its derivative, and determining binding between them, where the binding is indicative of HLA-A2 on the surface of the cell. The NY-ESO-1 peptides and analogues are useful therapeutically, for administration to a patient who is HLA-A2 positive and expresses NY-ESO-1 in connection with the pathology, as well as diagnostically, i.e. to determine if HLA-A2 positive cells are present, or if relevant CTLs are present. They are also useful for determining the presence of CTLs in a sample. The peptides are useful as T-cell sorters, when incorporated into immune trimers. The present sequence represents a NY-ESO-1 peptide that can bind to HLA-A2 molecule.

```
Query Match 100.0%; Score 57; DB 22; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 10; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;
```

1 LLMWITQCFL 10
| | | | | | | |
2 11mwitqcf1 11

SULT 13
B85298 AAB85298 standard; peptide: 11 AA.

AAB85298;
17-SEP-2001 (first entry)
HLA-A2 binding NY-ESO-1 peptide #1.
NY-ESO-1; human leukocyte antigen; HLA; lysis; cytolytic T cell; CTL;
HLA-A2; T-cell sorter; tumor; immune tetramer.

Homo sapiens .
WO200136453-A2 .

15 NOV 1000 0000-0100
08 -NOV -2000; 2000MO-US42010.
25 -MAY -2001 .

25-FEB-2000; 20000US-0514036.
29-SEP-2000; 20000US-0676005.

(LUDW-) LUDWIG INST CANCER RES.
(UYOX-) UNIV OXFORD.

Valmori D, Cerottini J, Romero P, Cerundolo V;

Novel isolated NY-ESO-1 nonapeptide useful for determining if a cell presents human leukocyte antigen-A2 molecule on its surface, binds to human leukocyte antigen molecules and provokes lysis by cytotoxic T

Example 1; Page 4 ; 38pp; English.

The invention provides NY-ESO-1 peptide derivatives which bind to human leukocyte antigen (HLA) molecules and provokes lysis by cytolytic T cells (CTLs). The NY-ESO-1 nonapeptide is of formula SLLMWITQX, where X is an amino acid having an uncharged polar side chain. The NY-ESO-1 peptide derivatives are useful for determining if a cell expresses an NY-ESO-1

molecule on its surface, by contacting a sample containing the cell with the peptide or its derivative, and determining binding between them, where the binding is indicative of HLA-A2 on the surface of the cell. The NY-ESO-1 peptides and analogues are useful therapeutically, for administration to a patient who is HLA-A2 positive and expresses NY-ESO-1 in connection with the pathology, as well as diagnostically, i.e. to determine if HLA-A2 positive cells are present, or if relevant CTLs are present. They are also useful for determining the presence of CTLs in a sample. The peptides are useful as T-cell sorters, when incorporated into immune trimers. The present sequence represents a NY-ESO-1 peptide that can bind to HLA-A2 molecule.

```

Query Match      100.0%; Score 57; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. NO. 0.0022;
Matches 10; Conservative 0; Mismatches 0;
Indels 0; Gaps 0

```

RESULT 14

ID AAE02119 standard; peptide; 11 AA.
XX
AC AAE02119;

xx OT 31-JUL-2001 (first entry)
xx DE NV-FESQ-1 human leukocyte antigen typing #1

KW Human; cytostatic; immunogen; NY-ESO-1; human leukocyte antigen;
HLA; CD8; cytotoxic T lymphocyte; cancer; carcinoma; melanoma; myeloma;
brain tumour; sarcoma; vaccine; gene therapy.

2D XX 26-APR-2001.
3F XX 19-OCT-2000: 2000W0-IIS28852

KX
PR 19-OCT-1999; 99US-0160374.
PR 01-FEB-2000; 2000US-0179570.

PA (LUDW-) LUDWIG INST CANCER RES.
XX Heidecker L, Van Den Eynde B, Boon-Falleur T, Brasseur F;

New antigenic peptides derived from MAGE-A12 polypeptides, useful for diagnosis and treatment of cancer such as bladder lung breast

PT brain, prostate and renal carcinomas -
KK Disclosure; Page 21; 69pp; English.
PS

The patent discloses antigenic peptides derived from MAGE-A12 protein and presented by human leukocyte antigens (HLAs). These antigenic peptides when presented by an antigen presenting cell having a HLA class I molecule, effectively induce the activation and proliferation of CD8+ cytotoxic T lymphocytes (CTLs). MAGE-A12 is useful for treating a subject having a disorder characterised by expression of MAGE-A12. The protein microarray comprising MAGE-A12 is useful for diagnosing a disorder, especially cancer, by determining the binding of an antibody, T lymphocytes or a HLA molecule isolated from the subject suspected of having the disorder characterised by the expression of MAGE-A12. MAGE-A12 is useful for treating cancers, including bladder cancer, testicular cancer, breast cancer, ovarian cancer, prostate cancer, head and neck cancer, lung cancer, liver cancer, and brain cancer.

neck, breast, colorectal carcinomas, myelomas, brain tumours, sarcomas, prostate and renal carcinomas and to produce antibodies. MAGE-A12 antibodies are useful for diagnosing disorders characterised by expression of MAGE-A12 immunogenic polypeptide. These MAGE-A12 peptides are used as vaccines. They are also used in gene therapy.

The present sequence is an antigenic peptide derived from NY-ESO-1. This peptide which is characteristic of tumours is presented by HLA-A2 MHC (major histocompatibility complex) and is recognised by CTLs.

XX SQ Sequence 11 AA;

	Query Match	Score	DB	Length
Best Local Matches	100.0%	22	11;	
Local Similarity	100.0%	No.	0.0022;	
Matches	10;	Mismatches	0;	
Conservative	0;	Indels	0;	
		Gaps	0;	

Qy 1 LLMWITQCFL 10
 ||||| | | | |
 Db 2 llmwitqcf1 11

RESULT 15
 AAU01536 ID AAU01536 standard; Peptide; 11 AA.

XX AC AAU01536;

XX DT 18-JUL-2001 (first entry)

XX DE Cytolytic T cell line stimulator peptide #1.

XX KW NY-ESO-1; human; tumour rejection antigen Precursor; SSX-2; MHC Class II;

KW major histocompatibility complex; helper T cell; HLA-DR; cancer;

KW human leukocyte antigen-determining region; disease progression;

KW disease regression; disease onset; body tissue; enzyme label;

KW radioactive label; monoclonal antibody; cytolytic T cell line.

XX OS Homo sapiens.

XX PN WO200123560-A2.

XX PD 05-APR-2001.

XX PF 26-SEP-2000; 2000WO-US26411.

XX PR 29-SEP-1999; 99US-0408036.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Tureci O, Sahin U, Pfreundschuh M;

XX DR 2001-266156/27.

XX PT Polypeptides binding to major histocompatibility complex Class II human

PT leukocyte antigen-determining region molecule having amino acid

PT sequence found in tumour rejection antigen precursor used for

PT stimulating proliferation of helper T cells.

XX PS Example 12; Page 17; 62pp; English.

XX The sequence represents a human NY-ESO-1 tumour rejection antigen precursor fragment which efficiently stimulates cytolytic T cell lines. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to major histocompatibility complex (MHC) Class II molecules such as human leukocyte antigen-determining region (HLA-DR) molecules and stimulate proliferation of helper T cells. The peptides can be administered to an HLA-DR positive subject in order to stimulate the helper T cells. An MHC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in free form is useful for this stimulation. The nucleic acid is useful for screening for a cancerous condition, which involves contacting a subject sample to a cell line transfected with the immunoreactive cell (helper T cell), where interaction is indicative of cancer. In addition, a sample from a patient (for example, a body fluid

CC or tissue) can be monitored for the amount of the complex present in the bloodstream. This is useful for determining regression, progression or onset of a cancerous condition. The method involves contacting the sample with a radioactive labelled or enzyme labelled monoclonal antibody which specifically binds with the complex.

XX SQ Sequence 11 AA;

	Query Match	Score	DB	Length
Best Local Matches	100.0%	No.	0.0022;	
Local Similarity	100.0%	Mismatches	0;	
Matches	10;	Conservative	0;	
		Indels	0;	
		Gaps	0;	

Qy 1 LLMWITQCFL 10
 ||||| | | | |
 Db 2 llmwitqcf1 11

Search completed: July 16, 2002, 07:45:50
 Job time: 358 sec

APPLICATION NUMBER: 08/937,263
 FILING DATE: September 15, 1997
 APPLICATION NUMBER: US 08/752,182
 FILING DATE: 03 -October-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, Norman D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5466 .3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-09-165-546A-7

Query Match 100.0%; Score 57; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLMWITQCFL 10
 Db 1 LLMWITQCFL 10

RESULT 2
 US-09-529-206-92
 ; Sequence 92, Application US/09529206
 ; GENERAL INFORMATION:
 ; APPLICANT: The Government of the United States of America as
 ; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
 ; TITLE OF INVENTION: Encoding Same
 ; FILE REFERENCE: 20264269PC
 ; CURRENT APPLICATION NUMBER: US/09/529,206
 ; CURRENT FILING DATE: 2000-06-13
 ; PRIOR APPLICATION NUMBER: US60/061,428
 ; PRIOR FILING DATE: 1997-10-08
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 92
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-529-206-92

Query Match 100.0%; Score 57; DB 19; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
 Db 1 LLMWITQCFL 10

Query Match 100.0%; Score 57; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
 Db 1 LLMWITQCFL 10

RESULT 3
 US-09-529-206A-92
 ; Sequence 92, Application US/09529206A
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang Rong, Fu
 ; APPLICANT: Rosenberg, Steven
 ; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
 ; TITLE OF INVENTION: Encoding Same
 ; FILE REFERENCE: 20264269US1
 ; CURRENT APPLICATION NUMBER: US/09/529,206A
 ; CURRENT FILING DATE: 2000-06-13
 ; PRIOR APPLICATION NUMBER: US60/061,428
 ; PRIOR FILING DATE: 1997-10-08
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 42
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

; PRIOR FILING DATE: 1997-10-08
 ; NUMBER OF SEQ ID NOS: 127
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 92
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-529-206A-92

Query Match 100.0%; Score 57; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
 Db 1 LLMWITQCFL 10

Query Match 100.0%; Score 57; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
 Db 1 LLMWITQCFL 10

RESULT 4
 US-09-529-206B-92
 ; Sequence 92, Application US/09529206B
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang Rong, Fu
 ; APPLICANT: Rosenberg, Steven
 ; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
 ; TITLE OF INVENTION: Encoding Same
 ; FILE REFERENCE: 20264269US1
 ; CURRENT APPLICATION NUMBER: US/09/529,206B
 ; CURRENT FILING DATE: 2000-06-13
 ; PRIOR APPLICATION NUMBER: PCT/US98/19609
 ; PRIOR FILING DATE: 1998-09-21
 ; PRIOR APPLICATION NUMBER: US60/061,428
 ; PRIOR FILING DATE: 1997-10-08
 ; NUMBER OF SEQ ID NOS: 127
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 92
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-529-206B-92

PCT-US00-04326-42

Query Match 100.0%; Score 57; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.11; Old, Lloyd, Ritter, Gerd
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
 1111111111
 Db 2 LLMWITQCFL 11

RESULT 6
 PCT-US99-06875-4 ; Sequence 4, Application PC/TUSS9906875
 ; GENERAL INFORMATION:
 ; APPLICANT: Stockert, Elisabeth; Jager, Elke; Knuth, Alexander;
 ; APPLICANT: Old, Lloyd J.
 ; TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
 ; TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
 ; TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
 ; TITLE OF INVENTION: THEREFROM
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US99/06875
 FILING DATE: 03-October-1996
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/937,263
 FILING DATE: September 15, 1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/752,182
 FILING DATE: 03-October-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, Norman D.

REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5466.3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-165-546A-4

Query Match 100.0%; Score 57; DB 15; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
 1111111111
 Db 2 LLMWITQCFL 11

RESULT 8
 US-09-336-091-41
 ; Sequence 41, Application US/09336091
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Snick, Jacques
 ; APPLICANT: Chaux, Pascal
 ; APPLICANT: Boon-Falleur, Thierry
 ; APPLICANT: van der Bruggen, Pierre
 ; TITLE OF INVENTION: MAGE-A1 PEPTIDES PRESENTED BY HLA CLASS
 ; FILE REFERENCE: L0461/7063
 ; CURRENT APPLICATION NUMBER: US/09/336,091
 ; CURRENT FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 41

Query Match 100.0%; Score 57; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 10
 1111111111
 Db 2 LLMWITQCFL 11

RESULT 7
 US-09-165-546A-4
 ; Sequence 4, Application US/09165546A

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; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-336-091-41

Query Match      100.0%; Score 57; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 LLMWITQCFL 10
Db   2 LLMWITQCFL 11

RESULT 11
US-09-440-621-1
; Sequence 1, Application US/09440621
; GENERAL INFORMATION:
; APPLICANT: Valmori, Danila
; APPLICANT: Cerottini, Jean-Charles
; APPLICANT: Romero, Pedro
; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
; FILE REFERENCE: LUD 5629
; CURRENT APPLICATION NUMBER: US/09/440,621
; CURRENT FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 09/165,546
; EARLIER FILING DATE: 1998-10-02
; EARLIER APPLICATION NUMBER: US 09/062,422
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: US 08/725,162
; EARLIER FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; US-09-440-621-1

Query Match      100.0%; Score 57; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 LLMWITQCFL 10
Db   2 LLMWITQCFL 11

RESULT 12
US-09-510-635A-4
; Sequence 4, Application US/09510635A
; GENERAL INFORMATION:
; APPLICANT: Bernard Leth, and Thierry Boon-Falleur
; TITLE OF INVENTION: ISOLATED GENOMIC SEQUENCES WHICH ENCODE NY-ESO-1 AND USES
; FILE REFERENCE: LUD 5633
; CURRENT APPLICATION NUMBER: US/09/510,635A
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-2
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-510-635A-4

Query Match      100.0%; Score 57; DB 19; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 LLMWITQCFL 10
Db   2 LLMWITQCFL 11

RESULT 10
US-09-408-036B-4
; Sequence 4, Application US/09408036B
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschatz, Michael
; TITLE OF INVENTION: Isolated Peptides Which Bind to MHC Class II Molecules and Uses
; FILE REFERENCE: LUD 5624
; CURRENT APPLICATION NUMBER: US/09/408,036B
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/165,546
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-408-036B-4

Query Match      100.0%; Score 57; DB 19; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 13
 US-09-574-749-33
 ; Sequence 33, Application US/09574749
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSENZWEIG, Michael
 ; APPLICANT: PYKETT, Mark J.
 ; APPLICANT: SCADDEN, David T.
 ; APPLICANT: POZNANSKY, Mark C.
 ; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
 ; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
 ; FILE REFERENCE: C1005/7006
 ; CURRENT APPLICATION NUMBER: US/09/574,749
 ; CURRENT FILING DATE: 2000-05-18
 ; PRIOR APPLICATION NUMBER: PCT/US99/26795
 ; PRIOR FILING DATE: 1999-11-12
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSEQ for Windows version 3.0
 ; SEQ ID NO 33
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Homo Sapiens source
 US-09-574-749-33

Query Match 100.0%; Score 57; DB 19; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLMWITQCFL 10
 |||||
 Db 2 LLMWITQCFL 11

Query Match 100.0%; Score 57; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLMWITQCFL 10
 |||||
 Db 2 LLMWITQCFL 11

RESULT 14
 US-09-676-005B-1
 ; Sequence 1, Application US/09676005B
 ; GENERAL INFORMATION:
 ; APPLICANT: Valmori, Danila
 ; APPLICANT: Cerrotini, Jean, Charels
 ; APPLICANT: Romero, Pedro
 ; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
 ; FILE REFERENCE: LUD 5629.2
 ; CURRENT APPLICATION NUMBER: US/09/676,005B
 ; CURRENT FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: US09/514,036
 ; PRIOR FILING DATE: 2000-02-05
 ; PRIOR APPLICATION NUMBER: US09/440,621
 ; PRIOR FILING DATE: 1999-11-15
 ; PRIOR APPLICATION NUMBER: US 09/165,546
 ; PRIOR FILING DATE: 1998-10-02
 ; PRIOR APPLICATION NUMBER: US 09/062,422
 ; PRIOR FILING DATE: 1998-04-17
 ; PRIOR APPLICATION NUMBER: US 08/725,162
 ; PRIOR FILING DATE: 1996-10-03
 ; NUMBER OF SEQ ID NOS: 27
 ; SEQ ID NO 1
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; US-09-676-005B-1

Query Match 100.0%; Score 57; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLMWITQCFL 10
 |||||
 Db 2 LLMWITQCFL 11

Search completed: July 16, 2002, 07:56:35
 Job time: 813 sec

Gencore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:43:42 ; Search time 63.47 Seconds
 (without alignments)
 17.524 Million cell updates/sec

Title: US-09-165-546A-7

Perfect score: 57

Sequence: 1 LLMWITQCFL 10

Scoring table: BILOSUM62
 Gapext 0.5

Searched: 344541 seqs, 111227333 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database :

Pending_Patents_AA_New:
 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
 7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	57	100.0	11	5	US-09-344-040C-130		Sequence 130, APP
2	57	100.0	11	5	US-09-574-749B-33		Sequence 33, Appl
3	57	100.0	11	6	US-10-117-277-130		Sequence 130, App
4	57	100.0	28	6	US-10-117-937-255		Sequence 255, App
5	57	100.0	180	1	PCT-US02-13994-30		Sequence 30, Appl
6	57	100.0	180	5	US-09-807-512-4		Sequence 4, Appl
7	57	100.0	180	5	US-09-807-512-8		Sequence 8, Appl
8	57	100.0	180	6	US-10-117-937-74		Sequence 74, Appl
9	57	100.0	180	6	US-10-117-937-75		Sequence 75, Appl
10	57	100.0	180	6	US-10-146-473-69		Sequence 69, Appl
11	53	93.0	9	5	US-09-344-040C-123		Sequence 123, APP
12	53	93.0	9	6	US-10-117-277-123		Sequence 123, APP
13	47	82.5	9	1	PCT-US02-05748-24		Sequence 24, Appl
14	47	82.5	9	5	US-09-344-040C-131		Sequence 131, APP
15	47	82.5	9	5	US-09-670-456A-1		Sequence 131, Appl
16	47	82.5	9	5	US-09-574-749B-34		Sequence 34, Appl
17	47	82.5	9	6	US-10-117-937-197		Sequence 197, App
18	47	82.5	9	6	US-10-117-277-131		Sequence 131, App
19	44	77.2	9	6	US-10-117-937-196		Sequence 196, App
20	38	66.7	9	1	PCT-US02-05748-25		Sequence 25, Appl
21	38	66.7	462	7	US-60-360-039-4233		Sequence 4233, AP
22	38	66.7	996	7	US-60-382-898-110		Sequence 110, APP
23	37	64.9	125	1	PCT-US02-09921-971		Sequence 971, APP
24	36	63.2	176	5	US-09-935-625-10391		Sequence 10391, A
25	36	63.2	205	5	US-09-935-625-10389		Sequence 10389, A
26	36	63.2	259	5	US-09-935-625-9112		Sequence 9112, AP

ALIGNMENTS

RESULT 1
 US-09-344-040C-130
 ; Sequence 130, Application US/09344040C
 ; GENERAL INFORMATION:
 ; APPLICANT: Tureci, Ozlem
 ; APPLICANT: Sahin, Ugur
 ; APPLICANT: Pfreundschuh, Michael
 ; APPLICANT: Ramensee, Hans Georg
 ; APPLICANT: Stevanovic, Stefan
 ; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining Presence of an SSX Gene, Peptides Derived From Said SSX Gene,
 ; TITLE OF INVENTION: Expression of an SSX Gene, and Uses Thereof
 ; TITLE OF INVENTION: Gene, and Uses Thereof
 ; FILE REFERENCE: LUD 5556.1
 ; CURRENT APPLICATION NUMBER: US/09/344,040C
 ; CURRENT FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: US 09/105, 839
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 08/851,130
 ; PRIOR FILING DATE: 1997-05-05
 ; NUMBER OF SEQ ID NOS: 132
 ; SEQ ID NO 130
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-344-040C-130

Query Match Best Local Similarity 100.0%; Score 57; DB 5; Length 11;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
 Db 2 LLMWITQCFL 11

RESULT 2
 US-09-574-749B-33
 ; Sequence 33, Application US/09574749B
 ; GENERAL INFORMATION:
 ; APPLICANT: ROSENZWEIG, Michael
 ; APPLICANT: PYKETT, Mark J.
 ; APPLICANT: SCADDEN, David T.
 ; APPLICANT: POZNANSKY, Mark C.
 ; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
 ; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
 ; TITLE OF INVENTION: DEVICES
 ; FILE REFERENCE: C1005/7012/KA/ERG
 ; CURRENT APPLICATION NUMBER: US/09/574,749B

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; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
; US-09-574-749B-33

Query Match      100.0%; Score 57; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 LLMWITQCFL 10
Db   2 LLMWITQCFL 11

RESULT 3
US-10-177-277-130
; Sequence 130, Application US/10177277
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determination of an SSX Gene, Peptides Derived From Said SSX Gene and Use Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO: 130
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-177-277-130

Query Match      100.0%; Score 57; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 LLMWITQCFL 10
Db   2 LLMWITQCFL 11

RESULT 4
US-10-117-937-255
; Sequence 255, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: Camel, An Alternative Translation Product of the Tumor
; TITLE OF INVENTION: Antigen-Lage 1
; TITLE OF INVENTION: Antigen-Lage 1

Query Match      100.0%; Score 57; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 LLMWITQCFL 10
Db   2 LLMWITQCFL 11

RESULT 5
PCT-US02-13994-30
; Sequence 30, Application PC/TUS0213994
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research
; APPLICANT: Cornell Research Foundation, Inc.
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; APPLICANT: Scanlan, Matthew
; APPLICANT: Stockert, Elisabeth
; TITLE OF INVENTION: COLON CANCER ANTIGEN PANEL
; FILE REFERENCE: L00461/70105WO(JRV)
; CURRENT APPLICATION NUMBER: PCT/US02/13994
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US 09/849,602
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 30
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US02-13994-30

Query Match      100.0%; Score 57; DB 1; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 LLMWITQCFL 10
Db   2 LLMWITQCFL 11

RESULT 6
US-09-807-512-4
; Sequence 4, Application US/09807512
; GENERAL INFORMATION:
; APPLICANT: Schrier, Peter I.
; APPLICANT: Arnoudse, Corlien
; APPLICANT: Heider, Karl-Heinz
; APPLICANT: Klade, Christoph
; TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
; TITLE OF INVENTION: Antigen-Lage 1
; TITLE OF INVENTION: Antigen-Lage 1

```

FILE REFERENCE: 0652.2200000
 CURRENT APPLICATION NUMBER: US/09/807,512
 CURRENT FILING DATE: 2001-04-16
 PRIOR APPLICATION NUMBER: PCT/EP99/07832
 PRIOR FILING DATE: 1999-10-15
 PRIOR APPLICATION NUMBER: EP 98119583.7
 PRIOR FILING DATE: 1998-10-16
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-807-512-4

Query Match 100.0%; Score 57; DB 5; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.046;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

QY 1 LLMWITQCFL 10
 |||||||
 Db 158 LLMWITQCFL 167

RESULT 7
 US-09-807-512-8
 Sequence 8, Application US/09807512
 GENERAL INFORMATION:
 APPLICANT: Schrier, Peter I.
 APPLICANT: Aarnoudse, Corlien
 APPLICANT: Heider, Karl-Heinz
 APPLICANT: Klade, Christoph
 TITLE OF INVENTION: Camel, An Alternative Translation Product of the Tumor
 TITLE OF INVENTION: Antigen-Lage 1
 FILE REFERENCE: 0652.2200000
 CURRENT APPLICATION NUMBER: US/09/807,512
 CURRENT FILING DATE: 2001-04-16
 PRIOR APPLICATION NUMBER: PCT/EP99/07832
 PRIOR FILING DATE: 1999-10-15
 PRIOR APPLICATION NUMBER: EP 98119583.7
 PRIOR FILING DATE: 1998-10-16
 NUMBER OF SEQ ID NOS: 28
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 8
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-807-512-8

Query Match 100.0%; Score 57; DB 5; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.046;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

QY 1 LLMWITQCFL 10
 |||||||
 Db 158 LLMWITQCFL 167

RESULT 8
 US-10-117-937-74
 Sequence 74, Application US/10117937
 GENERAL INFORMATION:
 APPLICANT: CTL IMMUNO THERAPIES CORP.
 APPLICANT: SIMARD, John, J.L.
 APPLICANT: DIAMOND, David, C.
 APPLICANT: LIU, Liping
 APPLICANT: XIE, Zhidong
 TITLE OF INVENTION: EPITOPE SEQUENCES
 FILE REFERENCE: CTLIMM.027A
 CURRENT APPLICATION NUMBER: US/10/117,937
 CURRENT FILING DATE: 2002-04-04
 PRIOR APPLICATION NUMBER: US 60/282,211
 PRIOR FILING DATE: 2001-04-06
 PRIOR APPLICATION NUMBER: US 60/337,017
 PRIOR FILING DATE: 2001-11-07
 PRIOR APPLICATION NUMBER: US 60/363,210
 PRIOR FILING DATE: 2002-03-07
 NUMBER OF SEQ ID NOS: 602
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 75
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-117-937-75

Query Match 100.0%; Score 57; DB 6; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.046;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

QY 1 LLMWITQCFL 10
 |||||||
 Db 158 LLMWITQCFL 167

RESULT 9
 US-10-117-937-75
 Sequence 75, Application US/10117937
 GENERAL INFORMATION:
 APPLICANT: CTL IMMUNO THERAPIES CORP.
 APPLICANT: SIMARD, John, J.L.
 APPLICANT: DIAMOND, David, C.
 APPLICANT: LIU, Liping
 APPLICANT: XIE, Zhidong
 TITLE OF INVENTION: EPITOPE SEQUENCES
 FILE REFERENCE: CTLIMM.027A
 CURRENT APPLICATION NUMBER: US/10/117,937
 CURRENT FILING DATE: 2002-04-04
 PRIOR APPLICATION NUMBER: US 60/282,211
 PRIOR FILING DATE: 2001-04-06
 PRIOR APPLICATION NUMBER: US 60/337,017
 PRIOR FILING DATE: 2001-11-07
 PRIOR APPLICATION NUMBER: US 60/363,210
 PRIOR FILING DATE: 2002-03-07
 NUMBER OF SEQ ID NOS: 602
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 75
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-117-937-75

Query Match 100.0%; Score 57; DB 6; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.046;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

QY 1 LLMWITQCFL 10
 |||||||
 Db 158 LLMWITQCFL 167

RESULT 10
 US-10-146-473-69
 Sequence 69, Application US/10146473
 GENERAL INFORMATION:
 APPLICANT: Scanlan, Matthew
 APPLICANT: Gout, Ivan
 APPLICANT: Stockert, Elisabeth
 APPLICANT: Gure, Ali
 APPLICANT: Chen, Yao-Tseng
 APPLICANT: Old, Lloyd
 TITLE OF INVENTION: Breast Cancer Antigens
 FILE REFERENCE: L00461/70130(JRV)

CURRENT APPLICATION NUMBER: US/10/146,473
 CURRENT FILING DATE: 2002-05-15
 PRIOR APPLICATION NUMBER: US 60/291,150
 PRIOR FILING DATE: 2001-05-15
 NUMBER OF SEQ ID NOS: 82
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 69
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-146-473-69

Query Match 100.0%; Score 57; DB 6; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.046;
 Matches 10; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 Qy 1 LLMWITQCFL 10
 Db 158 LLMWITQCFL 167

RESULT 11
 US-09-344-040C-123
 ; Sequence 123, Application US/09344040C
 ; GENERAL INFORMATION:
 ; APPLICANT: Tureci, Ozlem
 ; APPLICANT: Sahin, Ugur
 ; APPLICANT: Pfreundschuh, Michael
 ; APPLICANT: Ramensee, Hans Georg
 ; APPLICANT: Stevanovic, Stefan
 ; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determination of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof
 ; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof
 ; FILE REFERENCE: LUD 5556.1
 ; CURRENT APPLICATION NUMBER: US/09/344,040C
 ; CURRENT FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: US 09/105,839
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 08/851,130
 ; PRIOR FILING DATE: 1997-05-05
 ; NUMBER OF SEQ ID NOS: 132
 ; SEQ ID NO: 123
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-344-040C-123

Query Match 93.0%; Score 53; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 Qy 2 LLMWITQCFL 10
 Db 1 LLMWITQCFL 9

Query Match 82.5%; Score 47; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.1e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 LLMWITQC 8
 Db 2 LLMWITQC 9

RESULT 14

US-09-344-040C-131
 ; Sequence 131, Application US/09344040C
 ; GENERAL INFORMATION:
 ; APPLICANT: Tureci, Ozlem
 ; APPLICANT: Sahin, Ugur
 ; APPLICANT: Pfreundschuh, Michael
 ; APPLICANT: Ramensee, Hans Georg
 ; APPLICANT: Stevanovic, Stefan
 ; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determination of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof
 ; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof
 ; FILE REFERENCE: LUD 5556.1
 ; CURRENT APPLICATION NUMBER: US/09/344,040C
 ; CURRENT FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: US 09/105,839
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 08/851,130
 ; CURRENT APPLICATION NUMBER: US/10/177,277
 ; CURRENT FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: US/09/344,040
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: US 09/105,839
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 08/851,130
 ; NUMBER OF SEQ ID NOS: 132
 ; SEQ ID NO: 123
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-177-277-123

Query Match 93.0%; Score 53; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 Qy 2 LLMWITQCFL 10
 Db 1 LLMWITQCFL 9

Query Match 93.0%; Score 53; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 2 LLMWITQCFL 10
 Db 1 LLMWITQCFL 9

RESULT 13

PCT-US02-05748-24
 ; Sequence 24, Application PC/TUS0205748
 ; GENERAL INFORMATION:
 ; APPLICANT: Moriarty, Ann
 ; APPLICANT: Leturcq, Didier
 ; APPLICANT: Degraw, Juli
 ; APPLICANT: Heiskala, Marja
 ; APPLICANT: Peterson, Per
 ; APPLICANT: Jackson, Michael
 ; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
 ; FILE REFERENCE: ORT-1557
 ; CURRENT APPLICATION NUMBER: PCT/US02/05748
 ; CURRENT FILING DATE: 2002-02-19
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 24
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 PCT-US02-05748-24

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; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 131
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-131

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Query Match          82.5%;  Score 47;  DB 5;  Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches   8; Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Qy      1 LLMWITQC 8
Db      2 LLMWITQC 9

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RESULT 15
US-09-670-456A-1
; Sequence 1, Application US/09670456A
; GENERAL INFORMATION:
; LUD-5668-PCT
; APPLICANT: Gnjatic, Sacha
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA-C MOLECULES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: LUD 5668
; CURRENT APPLICATION NUMBER: US/09/670,456A
; CURRENT FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-670-456A-1

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Query Match          82.5%;  Score 47;  DB 5;  Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches   8; Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Qy      1 LLMWITQC 8
Db      2 LLMWITQC 9

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Search completed: July 16, 2002, 07:58:00
Job time: 858 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:41:32 ; Search time 45:25 Seconds
(without alignments)
5.398 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LIMWITQCFL 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:
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6: /cgn2_6/ptodata/2/iaa/backfile1.pep:
6:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	57	100.0	10	4	US-09-359-503-7	Sequence 7, Appli
2	57	100.0	11	4	US-09-183-931-42	Sequence 42, Appli
3	57	100.0	11	4	US-09-359-503-4	Sequence 4, Appli
4	57	100.0	11	4	US-09-062-422-4	Sequence 4, Appli
5	57	100.0	11	4	US-08-937-263B-4	Sequence 4, Appli
6	57	100.0	11	4	US-09-166-448-79	Sequence 79, Appli
7	57	100.0	180	2	US-08-791-495-7	Sequence 7, Appli
8	57	100.0	180	2	US-08-791-495-9	Sequence 9, Appli
9	57	100.0	180	4	US-08-937-263B-8	Sequence 8, Appli
10	47	82.5	9	4	US-09-183-931-43	Sequence 43, Appli
11	47	82.5	9	4	US-09-359-503-5	Sequence 5, Appli
12	47	82.5	9	4	US-09-062-422-5	Sequence 5, Appli
13	47	82.5	9	4	US-08-937-263B-5	Sequence 5, Appli
14	47	82.5	9	4	US-09-166-448-80	Sequence 80, Appli
15	35.5	62.3	20	2	US-08-934-915-84	Sequence 84, Appli
16	35	61.4	527	1	US-08-805-814-10	Sequence 10, Appli
17	35	61.4	527	1	US-08-844-815-10	Sequence 10, Appli
18	35	61.4	527	3	US-08-888-949-10	Sequence 10, Appli
19	35	61.4	527	4	US-08-888-950-10	Sequence 10, Appli
20	35	61.4	527	4	US-09-262-758-10	Sequence 10, Appli
21	35	61.4	527	5	PCT-US95-10284-10	Sequence 10, Appli
22	33	57.9	6	4	US-09-359-503-14	Sequence 14, Appli
23	33	57.9	6	4	US-09-062-422-7	Sequence 7, Appli
24	33	57.9	6	4	US-08-937-263B-7	Sequence 7, Appli
25	33	57.9	9	4	US-09-183-931-44	Sequence 44, Appli
26	33	57.9	9	4	US-09-359-503-6	Sequence 6, Appli
27	33	57.9	9	4	US-09-062-422-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-359-503-7

; Sequence 7, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, Alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid

TOPOLOGY: linear
US-09-359-503-7

Query Match 100.0%; Score 57; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 1 LLMWITQCFL 10

RESULT 2
US-09-183-931-42
Sequence 4.2, Application US/09183931C
Patent No. 6210886

GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Brasseur, Francis
APPLICANT: Boon-Falleur, Thierry

TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
FILE REFERENCE: LUD 5527.1-JEL/ES
CURRENT APPLICATION NUMBER: US/09/183,931C
CURRENT FILING DATE: 2000-02-28
EARLIER APPLICATION NUMBER: US 09/018,422
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 42
LENGTH: 11

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION:
US-09-183-931-42

Query Match 100.0%; Score 57; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 2 LLMWITQCFL 11

RESULT 3
US-09-359-503-4
Sequence 4, Application US/09359503
Patent No. 6251603

GENERAL INFORMATION:
APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, Alexander

TITLE OF INVENTION: Method for Determining Status Of A
Cancerous Condition By Determining Antibodies
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
SPECIFICATION-REF: 1
PCT NUMBER: US/09/359,503
DATE: July 23, 1999

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6251603man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-359-503-4

Query Match 100.0%; Score 57; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
Db 2 LLMWITQCFL 11

RESULT 4
US-09-062-422-4
Sequence 4, Application US/09062422
Patent No. 6252052

GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
APPLICANT: Old, Lloyd J.
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
APPLICANT: Old, Lloyd J.

TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
TITLE OF INVENTION: THEREFROM
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felice & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,422
FILING DATE:
ATTORNEY/AGENT INFORMATION:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6252052man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5466.3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-09-062-422-4

Query Match 100.0%; Score 57; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
 Db 2 LLMWITQCFL 11

RESULT 5
 US-08-937-263B-4
 ; Sequence 4, Application US/08937263B
 ; Patent No. 6274145

GENERAL INFORMATION:
 ; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
 ; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
 ; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
 ; TITLE OF INVENTION: ISOLATED NUCLEAR ACID MOLECULE
 ; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN,
 ; TITLE OF INVENTION: ITSELF, AND USES THEREOF
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski, L.L.P.
 ; STREET: 666 Fifth Avenue
 ; CITY: New York City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10103

COMPUTER READABLE FORM:
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/937,263B
 FILING DATE: September 15, 1997
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/725,182
 FILING DATE: October 3, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Sinn, Eric, Patent Agent
 REGISTRATION NUMBER: 40,177

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-3000
 TELEFAX: (212) 752-5958
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-937-263B-4

Query Match 100.0%; Score 57; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10

RESULT 6
 US-09-166-448-79
 ; Sequence 79, Application US/09166448
 ; Patent No. 6291430

GENERAL INFORMATION:
 ; APPLICANT: Chaux, Pascal
 ; APPLICANT: Vantomme, Valérie
 ; APPLICANT: Stroobant, Vincent
 ; APPLICANT: Boon-Falleur, Thierry
 ; APPLICANT: van der Bruggen, Pierre
 ; APPLICANT: Thielmans, Kris
 ; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS III MOLECULES
 ; FILE REFERENCE: L0461/7052
 ; CURRENT APPLICATION NUMBER: US/09/166,448
 ; CURRENT FILING DATE: 1998-10-05
 ; NUMBER OF SEQ ID NOS: 81
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 79
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-166-448-79

Query Match 100.0%; Score 57; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCFL 10
 Db 2 LLMWITQCFL 11

RESULT 7
 US-08-791-495-7
 ; Sequence 7, Application US/08791495
 ; Patent No. 5811519

GENERAL INFORMATION:
 ; APPLICANT: Leth, Bernard
 ; APPLICANT: Lucas, Sophie
 ; APPLICANT: De Smet, Charles
 ; APPLICANT: Godelaine, Danielle
 ; APPLICANT: Boon-Falleur, Thierry
 ; TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02210

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/791,495
 FILING DATE: August 11, 1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Van Amsterdam, John R.
 REGISTRATION NUMBER: 40,212
 REFERENCE/DOCKET NUMBER: L0461/7005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Van Amsterdam, John R.
 REGISTRATION NUMBER: 40,212
 REFERENCE/DOCKET NUMBER: L0461/7005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 180 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-791-495-7

Query Match	Score	DB	Length
Best Local Similarity	100.0%	2	180;
Matches	10;	Pred. No.	0.016;
QY	1 LLMWITQCFL 10	Mismatches	0;
Db	158 LLMWITQCFL 167	Indels	0;
		Gaps	0;

RESULT 8
 US-08-791-495-9
 Sequence 9, Application US/08791495
 Patent No. 5811519

GENERAL INFORMATION:

APPLICANT: Leth , Bernard
 APPLICANT: Lucas, Sophie
 APPLICANT: De Smet, Charles
 APPLICANT: Godellaïne, Danielle
 APPLICANT: Boon-Falleur, Thierry

TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 STREET: 600 Atlantic Avenue
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/791,495
 FILING DATE: 2000-02-28
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Van Amsterdam, John R.
 REGISTRATION NUMBER: 40,212
 REFERENCE/DOCKET NUMBER: L0461/7005

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 180 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-791-495-9

Query Match 100.0%; Score 57; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.016%; Mismatches 0%; Indels 0%; Gaps 0%;
 Matches 10; Conservative 0; Gaps 0%;
 QY 1 LLMWITQCFL 10
 Db 158 LLMWITQCFL 167

RESULT 9
 US-08-937-263B-8
 Query Match 100.0%; Score 57; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.016%; Mismatches 0%; Indels 0%; Gaps 0%;
 Matches 10; Conservative 0; Gaps 0%;
 QY 1 LLMWITQCFL 10
 Db 158 LLMWITQCFL 167

RESULT 9
 US-08-937-263B-8
 Query Match 100.0%; Score 57; DB 2; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.016%; Mismatches 0%; Indels 0%; Gaps 0%;
 Matches 10; Conservative 0; Gaps 0%;
 QY 1 LLMWITQCFL 10
 Db 158 LLMWITQCFL 167

GENERAL INFORMATION:
 TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
 FILE REFERENCE: LUD 5527.1-JEL/ES
 CURRENT APPLICATION NUMBER: US/09/183,931C
 CURRENT FILING DATE: 2000-02-28
 EARLIER APPLICATION NUMBER: US 09/018,422
 EARLIER FILING DATE: 1998 - 02 - 04
 NUMBER OF SEQ ID NOS: 44
 SEQ ID NO 43
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:

; OTHER INFORMATION:
; US-09-183-931-43

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQC 8
Db 2 LLMWITQC 9

RESULT 11
US-09-359-503-5
; Sequence 5, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, Alexander

; TITLE OF INVENTION: Method for Determining Status of A
; Title of Invention: Cancerous Condition By Determining Antibodies
; Title of Invention: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359, 503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165, 546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062, 422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937, 263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752, 182
; FILING DATE: 03-October-1996

ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6251603man D.
; REGISTRATION NUMBER: 30, 946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-09-062-422-5

Query Match 82.5%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQC 8
Db 2 LLMWITQC 9

RESULT 12
US-09-062-422-5
; Sequence 5, Application US/09062422
; Patent No. 6252052
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Old, Lloyd J.; Jager, Elke;
; APPLICANT: Knuth, Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF

NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fulbright & Jaworski, L.L.P.
 STREET: 666 Fifth Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10103

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/937,263B
 FILING DATE: September 15, 1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/725,182
 FILING DATE: October 3, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Sinn, Eric, Patent Agent
 REGISTRATION NUMBER: 40,177
 REFERENCE/DOCKET NUMBER: LUD 5466.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 318-3000
 TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 US-08-937-263B-5

Query Match 82.5%; Score 47; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
 Db 2 LLMWITQC 9

RESULT 14
 US-09-166-448-80
 ; Sequence 80, Application US/09166448
 ; Patent No. 6291430
 ; GENERAL INFORMATION:
 ; APPLICANT: Chaux, Pascal
 ; APPLICANT: Vantomme, Valrie
 ; APPLICANT: Stroobant, Vincent
 ; APPLICANT: Boon-Falleur, Thierry
 ; APPLICANT: van der Bruggen, Pierre
 ; APPLICANT: Thielemans, Kris
 ; APPLICANT: Corthals, Jurgen
 ; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
 ; FILE REFERENCE: L0461/7052
 ; CURRENT APPLICATION NUMBER: US/09/166,448
 ; CURRENT FILING DATE: 1998-10-05
 ; NUMBER OF SEQ ID NOS: 81
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 80
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-166-448-80

Query Match 82.5%; Score 47; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8

Search completed: July 16, 2002, 07:46:56
 Job time: 324 sec

Db 1 LLMWITAAAFRCFI 15

RESULT 15
 US-08-934-915-84
 ; Sequence 84, Application US/08934915
 ; Patent No. 5932412
 ; GENERAL INFORMATION:
 ; APPLICANT: DILLNER, JOAKIM
 ; APPLICANT: DILLNER, LENA
 ; APPLICANT: CHENG, HWEI-MING
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
 ; PAPILLOMAVIRUS 1, 5, 6, 8,
 ; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
 ; TITLE OF INVENTION: USEFUL IN IMMUNOCASSAY FOR
 ; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
 ; NUMBER OF SEQUENCES: 193
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MASON & ASSOCIATES, P.A.
 ; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
 ; CITY: CLEARWATER
 ; STATE: FLORIDA
 ; COUNTRY: U.S.A.
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows 3.0
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/934,915
 ; FILING DATE: 22-SEP-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/949,836
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: LOUISE A. FOUCHE
 ; REGISTRATION NUMBER: 37,133
 ; REFERENCE/DOCKET NUMBER: 1946.6
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 813-538-3800
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 84:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-934-915-84

Query Match 62.3%; Score 35.5; DB 2; Length 20;
 Best Local Similarity 46.7%; Pred. No. 6.3;
 Matches 7; Conservative 3; Mismatches 0; Indels 5; Gaps 1;
 QY 1 LLMWIT---QCFL 10
 Db 1 LLMWITAAAFRCFI 15

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:58:07 ; Search time 14.82 Seconds
 (without alignments)
 64.838 Million cell updates/sec

Title: US-09-165-546A-7
 Perfect score: 57
 Sequence: 1 LINWITQCFI 10
 Scoring table: BL0SUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 1099

Minimum DB seq length: 0
 Maximum DB seq length: 10Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR_71:
 1: pir1:
 2: pir2:
 3: pir3:
 4: pir4:
 * A; Accession: PT0289
 A; Molecule type: DNA
 A; Residues: 1-10 <YAM>
 A; Experimental source: B lymphocyte
 C; Keywords: heterotetramer; immunoglobulin

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	22	38.6	10	2	PT0289	Ig heavy chain CRD hypothetical prote
2	20	35.1	7	2	SC9652	glucuronosyltransferase - Rohde's
3	20	35.1	7	2	PX0008	cytochrome-c oxidase - Kluyvera
4	20	35.1	9	2	SC7241	diuretic neuropeptide - Rond's
5	20	35.1	10	2	T17075	seminal vesicle protein - malaria
6	19	33.3	8	2	S19288	hypothetical protein - conopressin G - co
7	18	31.6	9	2	A29477	lysine-conopressin - tryptophyllin, bas
8	18	31.6	9	2	T52974	cytochrome-c oxidase - common
9	17	29.8	5	2	B45525	isotocin - common oxytocin-related protein
10	17	29.8	7	2	S08606	hypothetical protein - Ig heavy chain CRD
11	17	29.8	9	2	A28495	t-cell receptor gamma - common
12	17	29.8	9	2	S39040	cytochrome-c oxidase - common
13	17	29.8	10	2	T13976	cytochrome-c oxidase - common
14	16	28.1	8	2	A41117	tryptophyllin, basic cytochrome oxidase - common
15	16	28.1	9	2	A61364	cytochrome-c oxidase - common
16	16	28.1	9	2	PC2021	cytochrome-c oxidase - common
17	16	28.1	10	2	S27873	cytochrome-c oxidase - common
18	16	28.1	10	2	PT0310	t-cell receptor gamma - common
19	16	28.1	10	2	E41946	cytochrome-c oxidase - common
20	16	28.1	10	2	T17057	cytochrome-c oxidase - common
21	16	28.1	10	2	T12303	cytochrome-c oxidase - common
22	16	28.1	10	2	T14019	cytochrome-c oxidase - common
23	16	28.1	10	2	T17060	cytochrome-c oxidase - common
24	16	28.1	10	2	T12325	cytochrome-c oxidase - common
25	16	28.1	10	2	T17072	cytochrome-c oxidase - common
26	16	28.1	10	2	T12312	cytochrome-c oxidase - common
27	15	26.3	6	2	F41946	t-cell receptor gamma - common
28	15	26.3	7	2	A61081	tryptophyllin, basic cytochrome oxidase - common
29	15	26.3	8	2	T13818	

RESULT	1	PT0289	Ig heavy chain CRD3 region (clone 4-109) - human (fragment)
C; Species:	Homo sapiens (man)	C; Date:	30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C; Accession:	PT0289	R; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.	J. Exp. Med. 173, 395-407, 1991
A; Title:	Preferential utilization of specific immunoglobulin heavy chain diversity and	A; Reference number:	MUID:91108337
A; Accession:	PT0289	A; Residues:	1-10 <YAM>
A; Molecule type:	DNA	C; Keywords:	heterotetramer; immunoglobulin
Query Match	38.6%	Score 22;	DB 2; Length 10;
Best Local Similarity	66.7%	Pred. No.	7.9e+02;
Matches	4;	Mismatches	1;
Conservative	4;	Indels	0;
Gaps	0;		
RESULT	2	S09652	hypothetical protein (aacc2 3' region) - Enterobacter cloacae (fragment)
C; Species:	Enterobacter cloacae	C; Date:	12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 08-Oct-1999
C; Accession:	S09652	R; Vliegenthart, J.S.; Ketelaar-van Gaalen, P.A.G.; van de Klundert, J.A.M.	Antimicrob. Agents Chemother. 33, 1153-1159, 1989
A; Title:	Nucleotide sequence of the aacc2 gene, a gentamicin resistance determinant in	A; Reference number:	S09651; MUID:90024972
A; Accession:	S09652	A; Molecule type:	DNA
A; Residues:	1-7 <VLI>	C; Keywords:	
Query Match	35.1%	Score 20;	DB 2; Length 7;
Best Local Similarity	40.0%	Pred. No.	2.8e+05;
Matches	2;	Mismatches	3;
Conservative	2;	Indels	0;
Gaps	0;		
RESULT	3		

PX0008
glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)
N;Alternate names: UDP-glucuronyltransferase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 07-Feb-1997
C;Accession: PX0008
R;Yokota, H.; Yuasa, A.; Sato, R.
J. Biochem. 104, 531-536, 1988
A;Title: Purification and properties of a form of UDP-glucuronyltransferase from liver n
A;Reference number: PX0008 ; MUID:89197852
A;Accession: PX0008
A;Molecule type: protein
A;Residues: 1-7 <YOK>
C;Keywords: glycosyltransferase; hexosyltransferase; liver

Query Match 35.1%; Score 20; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLMW 4
Db 3 LLWW 6

RESULT 4
S07241 Litorin - Rohde's leaf frog
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000
C;Accession: S07241
R;Barra, D.; Falconieri Erspamer, G.; Simmaco, M.; Bossa, F.; Melchiorri, P.; Erspamer,
FEBS Lett. 182, 53-56, 1985
A;Title: Rohdei-litorin: a new peptide from the skin of Phyllomedusa rohdei.
A;Reference number: S07241; MUID:85127560
A;Accession: S07241
A;Molecule type: protein
A;Residues: 1-9 <BAR>
C;Superfamily: gastrin-releasing peptide
C;Keywords: amidated carboxyl end; blocked amino end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidine carboxylic acid (Gln) #status experimental
F;9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 35.1%; Score 20; DB 2; Length 9;
Best Local Similarity 37.5%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 3 MWITQCFL 10
Db 2 LWATGHEM 9

RESULT 5
T17075 cytochrome-c oxidase (EC 1.9.3.1) chain I - Chamaeleo fischeri mitochondrion (fragment)
C;Species: mitochondrion Chamaeleo fischeri
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 22-Oct-1999
C;Accession: T17075
J. Mol. Evol. 44, 660-674, 1997
A;Title: Evolutionary shifts in three major structural features of the mitochondrial gen
A;Reference number: Z18674; MUID:97315309
A;Accession: T17075
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-10 <MAC>
A;Cross-references: EMBL:U82688; NID:g3603112; PID:g3603115; PIDN: AAC62275.1
C;Genetics:
A;Genome: mitochondrial
A;Note: <COI
C;Keywords: mitochondrion; oxidoreductase

Query Match 35.1%; Score 20; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 LLMW 5
Db 3 LLRWL 7

RESULT 6
S19288 acylase - Kluyvera cryocrescens
C;Species: Kluyvera cryocrescens
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S19288
R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.
Biochem. J. 280, 659-662, 1991
A;Title: Chemical modification of serine at the active site of penicillin acylase
A;Reference number: S19288; MUID:92109664
A;Accession: S19288
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <MAR>

Query Match 33.3%; Score 19; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 MWI 5
Db 3 MWV 5

RESULT 7
A2947 diuretic-neuropeptide F1 - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 31-Dec-1993
C;Accession: A29477
R;Proux, J.P.; Miller, C.A.; Li, J.P.; Carney, R.L.; Girardie, A.; Delaage, M.; Schoo
Biochem. Biophys. Res. Commun. 149, 180-186, 1987
A;Title: Identification of an arginine vasoressin-like diuretic hormone from Locusta
A;Reference number: A29477; MUID:88077077
A;Accession: A29477
A;Molecule type: protein
A;Residues: 1-9 <PRO>
A;Note: two neuropeptides, F1 and F2, were identified. F2 is an antiparallel dimer of
C;Keywords: neuropeptide

Query Match 31.6%; Score 18; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 5 ITQC 8
Db 3 ITNC 6

RESULT 8
I52974 seminal vesicle protein IV - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I52974
R;Teng, C.T.; Harris, S.E.
DNA 2, 105-111, 1983
A;Title: The seminal vesicle secretion IV gene: detection of S1 nuclease-sensitive si
A;Reference number: I52974 ; MUID:83261204
A;Accession: I52974
A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA
A;Residues: 1-9 <RESS>
A;Cross-references: GB:M27324; NID:g207124; PIDN:AAA63501.1; PID:g207125
C;Genetics:
A;Gene: SVSIV

Query Match 31.6%; Score 18; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 MWITQCFL 10
Db 1 MKLTSIPL 8

RESULT 9

B45525 actin I - malaria parasite (*Plasmodium falciparum*) (fragments)
C;Species: *Plasmodium falciparum*
C;Date: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C;Accession: B45525
R;Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoenmakers, Mol. Biochem. Parasitol. 35, 167-176, 1989
A;Title: Stage-specific expression and genomic organization of the actin genes of the malarial parasite
A;Reference number: A45525; MUID:89364996
A;Accession: B45525
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-5 <WES>
A;Cross-references: GB:J03988
A;Note: the authors translated the codon GAA for residue 3 as Gly
C;Comment: The actin I gene contains no introns.

Query Match 29.8%; Score 17; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 QCF 9
Db 3 ECF 5

RESULT 10

S08606 hypothetical protein 2 estrogen receptor 5'-region - chicken
C;Species: *Gallus gallus* (chicken)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 18-Aug-2000
C;Accession: S08606
R;Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Champon, P.
EMBO J. 5, 891-897, 1986
A;Title: The chicken oestrogen receptor sequence: homology with v-erbA and the human oestrogen receptor number: S07192; MUID:86247578
A;Accession: S08606
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <KRU>
A;Cross-references: EMBL:X03805; NID:g63378; PIDN:CAA27432.1; PID:g584490
C;Superfamily: unassigned leader peptides

Query Match 29.8%; Score 17; DB 2; Length 7;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 MWITQC 8
Db 1 MFLAHC 6

RESULT 11

A28495

Best Local Similarity 57.1%; Pred. No. 5.9e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 MWTOCF 9
 Db 1 MTTRWF 7

RESULT 14
 A41117
 acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)
 C;Species: Naja naja oxiana (Asian cobra, Oxus cobra)
 C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 23-Jun-1993
 C;Accession: A41117
 R;Kreienkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.
 PROG. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
 A;Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo a
 A;Reference number: A41117; MUID:91296772
 A;Accession: A41117
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-8 <KRE>
 C;Keywords: carboxylic ester hydrolase

Query Match 28.1%; Score 16; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 MW 4
 Db 4 MW 5

RESULT 15
 A61364
 isotocin - common carp
 C;Species: Cyprinus carpio (common carp)
 C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 20-Jun-2000
 C;Accession: A61364
 R;Acher, R.; Chauvet, J.; Chauvet, M.T.; Crepy, D.
 Comp. Biochem. Physiol. A 14, 245-254, 1965
 A;Title: Characterisation des hormones neurohypophysaires d'un poisson osseux d'eau douce
 A;Reference number: A61364
 A;Accession: A61364
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <ACH>
 C;Superfamily: oxytocin-neurophysin
 C;Keywords: amidated carboxyl end; neuropeptide; posterior pituitary
 F;9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.1%; Score 16; DB 2; Length 9;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 WITQC 8
 Db 2 YISNC 6

Search completed: July 16, 2002, 08:02:42
 Job time: 275 sec

Match

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 08:02:07 ; Search time 11.74 seconds

(without alignments)
 32.981 Million cell updates/sec

Title: US-09-165-546A-7
 Perfect score: 57
 Sequence: 1 LLMWITQCFL 10

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 349

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0⁸
 Maximum Match 100⁸
 Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	20	35.1	9	1	LITR_PHYRO	P08946 phylomedus
2	18	31.6	9	1	DNF1_LOCMI	P16339 locusta mig
3	17	29.8	9	1	CONO_CONGE	P05486 conus geogr
4	16	28.1	9	1	ISOT_CYPCA	P42993 cyprinus ca
5	16	28.1	9	1	OXYT_EISFO	P42998 eisenia foe
6	16	28.1	9	1	OXYT_RAJCL	P42994 raja clavat
7	15	26.3	5	1	UF01_MOUSE	P38639 mus musculu
8	15	26.3	9	1	MGMT_BOVIN	P29177 bos taurus
9	15	26.3	9	1	OXYA_SCYCA	P42996 scyliorhinu
10	15	26.3	9	1	OXYA_SQUAC	P42999 squalus aca
11	15	26.3	10	1	APE_CAPGI	P80474 capnocytoph
12	15	26.3	10	1	RCA_PINPS	P81084 pinus pinas
13	14	24.6	8	1	CPD1_ENTFEA	P13269 enterococcus
14	14	24.6	9	1	COVN_CONVE	P83047 conus ventr
15	14	24.6	9	1	OXYT_BUFR	P42995 bufo regula
16	14	24.6	9	1	OXYT_CYPCA	P23879 cyprinus ca
17	14	24.6	9	1	OXYT_RABIT	P32878 oryctolagus
18	14	24.6	9	1	OXYV_SQUAC	P43000 squalus aca
19	13	22.8	6	1	EI01_LITRU	P82096 litoria rub
20	13	22.8	9	1	D1_NEPPNO	P24816 nephrops no
21	13	22.8	9	1	LITO_LITAU	P08945 litoria aur
22	13	22.8	10	1	GON1_PETMA	P0367 oncorynchus
23	13	22.8	10	1	GON3_ONCKE	P27429 squalus aca
24	13	22.8	10	1	GONL_SQUAC	P13270 jatrophus mu
25	13	22.8	10	1	LABA_JATMU	P81533 microplitis
26	13	22.8	10	1	MP2_MICOC	P55962 nicotiana t
27	13	22.8	10	1	NO40_TOBAC	P80901 methanobacter
28	13	22.8	10	1	PORB_METTM	P20104 enterooccus
29	12	21.1	7	1	CCF1_ENTFA	P35919 achatina fu
30	12	21.1	7	1	WWA1_ACHFU	P35920 achatina fu
31	12	21.1	7	1	WWA2_ACHFU	P35921 achatina fu
32	12	21.1	7	1	WWA3_ACHFU	P18691 thunnius alb
33	12	21.1	8	1	AC1_THUAL	

ALIGNMENTS

P30369	macropus eu	34	12	21.1	8	1	CCKN_MACEU
P38556	carcinus ma	35	12	21.1	9	1	CCAP_CARMA
P05487	conus stria	36	12	21.1	9	1	CONO_CONST
P42997	scyliorhinu	37	12	21.1	9	1	OXYF_SCYCA
P80027	octopus vul	38	12	21.1	9	1	OXYT_OCTVU
P56264	litoria xan	39	12	21.1	10	1	CAER_LITXA
P18523	manduca sex	40	12	21.1	10	1	FARP_MANSE
P18110	romalea mic	41	12	21.1	10	1	HTF1_ROMMI
P11385	carausius m	42	12	21.1	10	1	HTF2_CARMO
P10939	nauphoeta c	43	12	21.1	10	1	HTF_NAUCI
P58649	octopus min	44	11	19.3	4	1	OCP3_OCTMI
P30425	bothrops in	45	11	19.3	5	1	BPP7_BOTIN

RESULT 1							
ID	LITR_PHYRO	STANDARD;	PRT;	9 AA.			
P08946;				AC			
DT	01-NOV-1988	(Rel. 09,	Created)	DT	01-FEB-1994	(Rel. 28,	Last sequence update)
DT	01-MAR-2002	(Rel. 41,	Last annotation update)	DE	Rhodei-litorin.		
OS	Phyllomedusa rohdei (Rohde's leaf frog).						
OC	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;						
OC	Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;						
OC	Phyllomedusa.						
RN	[1]						
RP	SEQUENCE.						
RX	MEDLINE=85127560; PubMed=3838283;						
RA	Barra D., Ersperer G.F., Simmacco M., Bossa F., Melchiorri P.,						
RA	Ersperer V.;						
RT	"Rohdei-litorin: a new peptide from the skin of Phyllomedusa rohdei."						
RL	FEBS Lett. 182:53-56(1985).						
CC	-!- SUBCELLULAR LOCATION: Secreted.						
CC	-!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN FAMILY.						
CC							
DR	P07241; S07241.						
DR	InterPro; IPR000874; Bombesin.						
DR	PFam; PF02044; Bombesin; 1.						
DR	PROSITE; PS0257; BOMBESIN; 1.						
KW	Bombesin family; Amidation.						
FT	MOD_RES	1	1				
FT	MOD_RES	9	9				
SQ	SEQUENCE	9 AA;	1090 MW;	4ECCC1E861ADC377 CRC64;			
Query Match	35.18;	Score 20;	DB 1;	Length 9;			
Best Local Similarity	37.58;	Pred. No. 1.e+05;					
Matches	3;	Conservative	2;	Mismatches	3;	Indels	0;
Gaps	0;						
RESULT 2							
ID	DNF1_LOCMI	STANDARD;	PRT;	9 AA.			
AC	P16339;						
DT	01-AUG-1990	(Rel. 15,	Created)	DT	01-AUG-1990	(Rel. 15,	Last sequence update)
DT	15-DEC-1998	(Rel. 37,	Last annotation update)	DE	Locupressin (Diuretic neuropeptide F1/F2).		
OS	Locusta migratoria (Migratory locust).						
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;						
OC	Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;						
OC	Acridomorpha; Acriidoidea; Acrididae; Locusta.						
OX	[1]						
RN							

RP SEQUENCE.
 RC TISSUE=Suboesophageal ganglion, and thoracic ganglion;
 RX MEDLINE=88077077; PubMed=3689410;
 RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
 RA Delaage M., Schooley D.A.;
 RT "Identification of an arginine vasopressin-like diuretic hormone from
 Locusta migratoria.";
 RL Biochem. Biophys. Res. Commun. 149:180-186(1987).
 CC -!- FUNCTION: DIURETIC HORMONE.
 CC -!- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR; A29477; A29477.
 DR InterPro; IPR000981; Neurhypophys_horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT DISULFID 1 6 IN F1.
 FT DISULFID 1 1 INTERCHAIN (WITH C-6') (IN F2).
 FT DISULFID 6 6 INTERCHAIN (WITH C-1') (IN F2).
 MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 31.6%; Score 18; DB 1; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ITCQ 8
 Db 3 ITNC 6

RESULT 3 CONO_CONGE
 ID CONO_CONGE STANDARD; PRT; 9 AA.
 AC P05486;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DE LYS-conopeptides in G.
 OS Conus geographus (Geography cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6491;
 RN SEQUENCE.

RX MEDLINE=88058932; PubMed=3680228;
 RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
 RA Gray W.R., Olivera B.M.;
 RT "Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from Conus geographus and Conus straitus venoms.";
 RL J. Biol. Chem. 262:15821-15824(1987).
 RN REVIEW.
 RX MEDLINE=89024586; PubMed=3052286;
 RA Gray W.R., Olivera B.M., Cruz L.J.;
 RT "Peptide toxins from venomous Conus snails.";
 RL Annu. Rev. Biochem. 57:665-700(1988).
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR; A28495; A28495.
 DR InterPro; IPR000981; Neurhypophys_horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1037 MW; D4FC276EB454 0059 CRC64;

QY 8 CFL 10
 Db 1 CFI 3

RESULT 4 ISOT_CYPCA
 ID ISOT_CYPCA STANDARD; PRT; 9 AA.
 AC P42993;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Isotocin.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE.
 RC Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
 RA RT "Characterization of neurohypophyseal hormones from a fresh water bony fish, the carp (Cyprinus carpio). Comparison with hormones from sea water bony fishes";
 RL Comp. Biochem. Physiol. 14:245-254 (1965).
 CC -!- FUNCTION: ANTIDIURETIC HORMONE.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR; A61364; A61364.
 DR InterPro; IPR000981; Neurhypophys_horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
 FT DISULFID 1 6
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 969 MW; 17FF476EB455B04B CRC64;

Query Match 28.1%; Score 16; DB 1; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WITQC 8
 Db 2 YISNC 6

RESULT 5 OXYT_EISFO
 ID OXYT_EISFO STANDARD; PRT; 9 AA.
 AC P42998;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Annetocin.
 OS Eisentia foetida (Common branding worm) (Common dung-worm).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
 OC Lumbricina; Lumbriidae; Eisentia.
 OX NCBI_TaxID=6396;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE=94121660; PubMed=8292046;
 RA Oumi T., Ukena K., Minakata H., Ikeda T., Fujita T., Minakata H.,
 RA Nomoto K.;
 RT "Annetocin: an oxytocin-related peptide isolated from the earthworm, Eisentia foetida.";
 RL Biochem. Biophys. Res. Commun. 198:393-399 (1994).
 CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
 CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
 CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
 CC NEPHRIDIAL FUNCTION.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

Query Match 29.8%; Score 17; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DR PIR; PC2021; PC2021; Neurhypophys_horm.
 DR InterPro; IPR000981; Neurhypophys_horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEURHYPOPHYS_HORM; FALSE_NEG.
 KW Hormone; Amidation.
 FT DISULFID 1 6 AMIDATION.
 FT MOD_RES 9 9 MW; D4EEB76EB45412C9 CRC64;
 SQ SEQUENCE 9 AA; 996 MW; 7364087043100000 CRC64;

Query Match 28.1%; Score 16; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CFL 10
 Db 1 CFV 3

RESULT 6
 ID OXYT_RAJCL STANDARD; PRT; 9 AA.
 AC P42994;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Glumitocin.
 OS Raja clavata (Thornback ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 RT "Phylogeny of neurohypophyseal Peptides: isolation of a new hormone,
 glumitocin (Ser 4-Gln 8-oxytocin) present in a cartilaginous fish,
 the ray (Raja clavata).";
 RT Biochim. Biophys. Acta 107:393-396 (1965).
 RL Biochim. Biophys. Acta 107:393-396 (1965).
 CC -!- FUNCTION: ANTIIDIURETIC HORMONE.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR Acher R., Chauvet J., Crepy D.;
 DR InterPro; IPR000981; Neurhypophys_horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEURHYPOPHYS_HORM; 1.
 KW Hormone; Amidation.
 FT DISULFID 1 6 AMIDATION.
 FT MOD_RES 9 9 MW; 17E9C76EB455B04B CRC64;
 SQ SEQUENCE 9 AA; 984 MW; 325171A720476047 CRC64;

Query Match 28.1%; Score 16; DB 1; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1e+05;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 WITQC 8
 Db 2 YISNC 6

RESULT 7
 ID UF01_MOUSE STANDARD; PRT; 5 AA.
 AC P38639;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]

RP SEQUENCE.
 RC TISSUE=Fibroblast; PubMed=7523108;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familiar and novel murine proteins
 using preparative two-dimensional gel electrophoresis.";
 RT Electrophoresis 15:735-745 (1994).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.6, ITS MW IS: 19 kDa.
 FT NON_TER 5 5
 SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 26.3%; Score 15; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WI 5
 Db 1 WI 2

RESULT 8
 ID MGMT_BOVIN STANDARD; PRT; 9 AA.
 AC P29177;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-methylguanine-DNA methyltransferase) (Fragment).
 DE Methylguanine-DNA methyltransferase (Fragment).
 GN MGMT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TAXID=9913;
 OX [1]
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thymus;
 RX MEDLINE=90174912; PubMed=2308822;
 RA Rydberg B., Hall J., Karran P.;
 RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
 methyltransferase.";
 RT Nucleic Acids Res. 18:17-21(1990).
 RL -!- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY
 CC TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE
 CC RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS
 CC IRREVERSIBLY INACTIVATED.
 CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + protein
 CC [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein
 CC S-methyl-L-cysteine.
 CC -!- SIMILARITY: WITH SEGMENTS OF E.COLI ADA AND OGT METHYLTRANSFERASE
 CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
 CC DR InterPro; IPR001497; Methyltransf_1.
 CC DR PROSITE; PS00374; MGMT; PARTIAL.
 CC KW DNA repair; Transferase; Methyltransferase.
 FT NON_TER 1 1
 FT ACT_SITE 9 9
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 26.3%; Score 15; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ITQC 8
 Db 6 LTPC 9

RESULT 9

OXYA_SCYCA ID OXYA_SCYCA STANDARD; PRT; 9 AA.
AC P42996;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Asvatocin.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark);
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Scyliorhinidae; scyliorhinus.
NCBI_TaxID=7830;
[1]
RN SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauvet M.-T., Achter R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
fishes: asvatocin and phasvatocin, two oxytocin-like peptides
isolated from the spotted dogfish (*Scyliorhinus caniculus*).";
RT Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
CC InterPro; IPR000981; Neurhypophys_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6 AMIDATION.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB44404B CRC64;

Query Match 26.3%; Score 15; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 4 WITQC 8
Db 2 YINNC 6

RESULT 10 OXYA_SQUAC ID OXYA_SQUAC STANDARD; PRT; 9 AA.
AC P42999;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Aspartocin (Aspargtocin).
OS Squalus acanthias (spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalidae; Squaloidei; Squalus; Squalus.
NCBI_TaxID=7797;
[1]
RN SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Achter R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
isolated from a cartilaginous fish, *Squalus acanthias*.";
RL Eur. J. Biochem. 29:12-19(1972).
RN SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Achter R., Chauvet J., Chauvet M.-T.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
spiny dog-fish (*Squalus acanthias*).";
RL C. R. Acad. Sci. I., D, Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro; IPR000981; Neurhypophys_horm.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.

FT DISULFID 1 6 AMIDATION.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 996 MW; 17F8376EB44404B CRC64;

Query Match 26.3%; Score 15; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 4 WITQC 8
Db 2 YINNC 6

RESULT 11 APE_CAPGI ID APE_CAPGI STANDARD; PRT; 10 AA.
AC P80474;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Aminopeptidase (EC 3.4.11.-) (Fragment).
OS Capnocytophaga gingivalis.
OC Bacteria; CFB group; Flavobacteria; Flavobacteriaceae; Capnocytophaga.
NCBI_TaxID=1017;
[1]
RN SEQUENCE.
RC STRAIN=ATCC 33624;
RX MEDLINE=96118234; PubMed=8574402;
RA Spratt D.A., Greenman J., Schaffer A.G.;
RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence
factor.";
RL Microbiology 141:3087-3093(1995).
CC -!- FUNCTION: AMINOPEPTIDASE WHICH HYDROLYZES SUBSTRATES WITH FREE N-
TERMINAL AMINO ACID RESIDUES BUT NOT N-TERMINAL BLOCKED ONES.
CC OPTIMUM ACTIVITY IS MEASURED AT PH 7.5. MAY BE IMPORTANT IN THE
CC NUTRITION AND PATHOGENESIS OF THE ORGANISM IN THE HUMAN ORAL
CC CAVITY.
CC -!- COFACTOR: REQUIRES MAGNESIUM OR CALCIUM.
KW Hydrolase; Aminopeptidase; Magnesium; Calcium.

FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1306 MW; 00C0A6DB43772694 CRC64;

Query Match 26.3%; Score 15; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 4.1e+03;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 LMW 4
Db 4 MLW 6

RESULT 12 RCA_PINPS ID RCA_PINPS STANDARD; PRT; 10 AA.
AC P81084;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable ribulose bisphosphate carboxylase/oxygenase activase (RuBisCO
activase) (RA) (Water stress responsive protein 4) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
[1]
RN SEQUENCE.
RX MEDLINE=98418576; PubMed=9747804;
RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water-deficit-responsive proteins in maritime pine.";

RL Plant Mol. Biol. 38:587-596(1998).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahman N., Kremer A.,
 Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- FUNCTION: ACTIVATION OF RUBISCO (RIBULOSE-1,5-BISPHOSPHATE
 CARBOXYLASE/OXYGENASE; EC 4.1.1.39) INVOLVES THE ATP-DEPENDENT
 CARBOXYLATION OF THE EPSILON-AMINO GROUP OF LYSINE LEADING TO A
 CARBAMATE STRUCTURE (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Chloroplast stroma (By similarity).
 CC -!- INDUCTION: BY WATER STRESS.
 CC -!- SIMILARITY: BELONGS TO THE RUBISCO ACTIVASE FAMILY.
 KW Chloroplast; ATP-binding.
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1171 MW; COA506D2C72B1EA6 CRC64;

Query Match 26.3%; Score 15; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 4.1e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 QCFL 10
 |||
 Db 3 QCFL 6

RESULT_13
 CPD1_ENTFA STANDARD; PRT; 8 AA.
 ID CPD1_ENTFA STANDARD;
 AC P13269;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CPD1.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
 OC Enterococcus.
 RN NCBI_TAXID=1351;
 RP SEQUENCE.
 RX MEDLINE=85040388; PubMed=6436978;
 RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
 RA Craig R.A., Clewell D.B.;
 RT "Isolation and structure of bacterial sex pheromone, CPD1.";
 RL Science 226:849-850(1984).
 CC -!- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC BACTERIOCIN PLASMID PPD1.
 KW Pheromone.
 SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 24.6%; Score 14; DB 1; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+05;
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWIT 6
 ||:::
 Db 2 LVMFLS 7

RESULT_14
 COVN_CONVE STANDARD; PRT; 9 AA.
 ID COVN_CONVE STANDARD;
 AC P83047;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Contryphan-Vn.
 OS Conus ventricosus (Mediterranean cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 Neogastropoda; Conoidea; Conidae; Conus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Raybaudi Massilia G., Schinina M.E., Ascenzi P., Politicelli F.;
 RT "Contryphan-Vn: a novel peptide from the venom of the Mediterranean
 vermivorous marine snail Conus ventricosus.";
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.
 CC -!- TISSUE SPECIFICITY: Venom.
 KW Amidation; Venom; D-amino acid.
 FT DISULFID 3 9
 FT MOD_RES 5 5
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 1091 MW; 8D38676323676EBA CRC64;

Query Match 24.6%; Score 14; DB 1; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WITQC 8
 |||
 Db 5 WKWMC 9

RESULT_15
 OXYT_BUFR STANDARD; PRT; 9 AA.
 ID OXYT_BUFR STANDARD;
 AC P42995;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Seritocin.
 OS Bufo regularis (Leopard toad).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;
 OC Bufo.
 RN NCBI_TAXID=8390;
 RP SEQUENCE.
 RC TISSUE=Pituitary neurointermediate lobe;
 RX MEDLINE=96059313; PubMed=7591488;
 RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Achter R.;
 RT "A new neurohypophysial peptide, seritocin ((Ser5,Ile8)-oxytocin),
 identified in a dryness-resistant African toad, Bufo regularis.";
 RL Int. J. Pept. Protein Res. 45:482-487(1995).
 CC -!- FUNCTION: DEVOID OF OXYTOCIC ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR InterPro IPR000981; Neurhypophys_horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
 KW Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 983 MW; 17FF476EA5A6D04B CRC64;

Query Match 24.6%; Score 14; DB 1; Length 9;
 Best Local Similarity 33.3%; Pred. No. 1e+05;
 Matches 1; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 8 CFL 10
 ||:
 Db 1 CYI 3

Search completed: July 16, 2002, 08:06:14
 Job time: 247 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 08:01:32 ; search time 26.12 Seconds
 (without alignments)
 66.231 Million cell updates/sec

Title: US-09-165-546A-7
 Perfect score: 57
 Sequence: 1 LMMWITQCFL 10

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 1088

Minimum DB seq length: 0
 Maximum DB seq length: 10

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTREMBL_19;*

- 1: sp_archaea;*
- 2: sp_bacteria;*
- 3: sp_fungi;*
- 4: sp_human;*
- 5: sp_invertebrate;*
- 6: sp_mammal;*
- 7: sp_mhc;*
- 8: sp_organelle;*
- 9: sp_phage;*
- 10: sp_plant;*
- 11: sp_rodont;*
- 12: sp_virus;*
- 13: sp_vertbrate;*
- 14: sp_unclassified;*
- 15: sp_rvirus;*
- 16: sp_bacteriap;*
- 17: sp_archeap;*

O9et16 mesocricetus auratus 17 16 28.1 8 11 O9ET16
 Q99mn0 mus musculus 18 16 28.1 8 11 Q9MN0
 Q62721 rattus norvegicus 19 16 28.1 8 11 O62721
 Q9r9c4 borrelia burgdorferi 20 16 28.1 9 2 Q9R9C4
 Q9h3y3 homo sapiens 21 16 28.1 9 4 Q9H3Y3
 Q934s1 thermus thermophilus 22 16 28.1 10 2 Q934S1
 Q25355 locusta migratoria 23 16 28.1 10 5 Q25355
 Q25356 locusta migratoria 24 16 28.1 10 5 Q25356
 Q9tr47 bos taurus 25 16 28.1 10 6 Q9tR47
 Q9zyv3 dipsosaurus dorsalis 26 16 28.1 10 8 Q9zyv3
 Q9zyu4 sceloporus magister 27 16 28.1 10 8 Q9ZYU4
 Q9zyt2 leiocephalus carinatus 28 16 28.1 10 8 Q9ZYT2
 P922707 platysaurus broadleyi 29 16 28.1 10 8 P92707
 P92632 eremias graniticolus 30 16 28.1 10 8 P92632
 Q9891 crotaphytus wislizenii 31 16 28.1 10 8 Q9891
 Q9894 gambelia wislizenii 32 16 28.1 10 8 Q9894
 Q9909 sauromalus occidentalis 33 16 28.1 10 8 Q9909
 Q9t8g5 liolaemus olrogii 34 16 28.1 10 8 Q9t8G5
 Q9b4x0 notophthalmus maculatus 35 16 28.1 10 8 Q9B4X0
 Q958k9 rana boylii 36 16 28.1 10 8 Q958K9
 Q61807 mus musculus 37 16 28.1 10 11 Q61807
 Q9e8q4 beet root 38 15 26.3 8 12 Q9E8Q4
 Q9d5n5 beet root 39 15 26.3 8 12 Q9D5N5
 Q99887 homo sapiens 40 15 26.3 9 4 Q99887
 Q94vi8 varanus eres 41 15 26.3 9 8 Q94Vi8
 Q94vh4 varanus glaucomelas 42 15 26.3 9 8 Q94VH4
 Q94vel varanus meridionalis 43 15 26.3 9 8 Q94VE1
 Q94vd8 varanus niloticus 44 15 26.3 9 8 Q94VD8
 Q38366 bacteriophaga 45 15 26.3 9 9 Q38366

ALIGNMENTS

RESULT 1
 ID 085406 PRELIMINARY;
 AC 085406; ID 085406; PRELIMINARY;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 1.0 KDA PROTEIN (FRAGMENT).
 OS Coxiella burnetii.
 OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
 OC Coxiella group; Coxiella.
 OX NCBI_TAXID=777;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NINE MILE PHASE I;
 RX MEDLINE=9834442; PubMed=9683477;
 RA Willems H., Jaeger C., Baljer G.;
 RT "Physical and genetic map of the obligate intracellular bacterium
 Coxiella burnetii."
 RL J. Bacteriol. 180:3816-3822(1998).
 DR EMBL; AF064963; AAD099471; -.
 KW Hypothetical protein.
 FT NON_TER 1 1 1
 SQ SEQUENCE 8 AA; 993 MW; 046B5AA453772727 CRC64;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	36.8	8	085406	O85406 coxiella bu
2	21	36.8	8	Q15890	Q15890 homo sapien
3	20	35.1	8	Q9VRD2	Q9vrD2 drosophila
4	20	35.1	10	Q79912	Q79912 chamaeleo f
5	20	35.1	10	Q9G697	Q9G697 chamaeleo d
6	19	33.3	10	Q9n1X1	Q9n1X1 equus caballus
7	19	33.3	10	Q9esu5	Q9esu5 mus musculus
8	17	29.8	9	Q96QA7	Q96qa7 homo sapien
9	17	29.8	9	Q9TG98	Q9tg98 shinisaurus
10	17	29.8	10	P92616	P92616 cnemidophor
11	17	29.8	10	Q94VJ4	Q94vj4 varanus bengalensis
12	17	29.8	10	Q9et18	Q9et18 mus spreatus
13	17	29.8	10	Q15890	Q15890 mus caroli
14	16	28.1	8	AC	Q15890
15	16	28.1	8	PRT;	PRT;
16	16	28.1	8	PRELIMINARY;	PRELIMINARY;

DT	01-NOV-1996 (TREMBLrel. 01, Created)	RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nixon K.A., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Purvi V., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Purvi V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of <i>Drosophila melanogaster</i> ."; RT Science 287:2185-2195 (2000).
OS	Homo sapiens (Human).;	RA	"Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries.";
OC	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.;	RA	Hum. Mol. Genet. 0:0-0 (1995).
OC	NCBI_TaxID=9606;	RA	DR EMBL; L32083; AAA73880.1; -.
FT	SEQUENCE FROM N.A. TISSUE=PLACENTA;	RA	DR FLYBase; FBgn0040648; CG11666.
FT	Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M., Chnault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y., Caskey C.T.H.; "Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries.";	RA	SQ SEQUENCE 8 AA; 975 MW; 605EA6C5BEEA5A2D3 CRC64;
FT	Hum. Mol. Genet. 0:0-0 (1995).	RA	Query Match Score 20; DB 5; Length 8;
FT	EMBL; L32083; AAA73880.1; -.	RA	Best Local Similarity 100.0%; Pred. No. 5.6e+05; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT	NON_TER	RA	Qy 3 MWI 5 Db 1 MWI 3
FT	NON_TER	RA	RESULT 4 079912 PRELIMINARY; ID 079912; PRT; 10 AA.
FT	SEQUENCE 8 AA; 975 MW; 605EA6C5BEEA5A2D3 CRC64;	RA	AC 079912; DT 01-NOV-1998 (TREMBLrel. 08, Created) DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update) DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
FT	SEQUENCE FROM N.A. STRAIN=BERKELEY;	RA	DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT). COI.
FT	SEQUENCE FROM N.A. STRAIN=BERKELEY;	RA	GN Chamaeleo fischeri. OG Mitochondrion. OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
FT	SEQUENCE FROM N.A. STRAIN=BERKELEY;	RA	RN (1) NCBI_TAXID=51755; RN SEQUENCE FROM N.A. MEDLINE=97315309; PubMed=9169559; RN Macej J.R., Larson A., Ananjeva N.B., Papenfuss T.J.; RT "Evolutionary shifts in three major structural features of the mitochondrial genome among iguanian lizards."; RN J. MOI. EVOl. 4:660-674 (1997). DR EMBL; U82688; AAC62275.1; -.
FT	SEQUENCE FROM N.A. STRAIN=BERKELEY;	RA	KW Mitochondrion. FT NON_TER 10 SQ SEQUENCE 10 AA; 1319 MW; 5E218E2733640727 CRC64;
FT	SEQUENCE FROM N.A. STRAIN=BERKELEY;	RA	Qy 1 LLMWI 5 Db 3 LLRWL 7
FT	SEQUENCE FROM N.A. STRAIN=BERKELEY;	RA	Query Match Score 20; DB 8; Length 10;
FT	SEQUENCE FROM N.A. STRAIN=BERKELEY;	RA	Best Local Similarity 60.0%; Pred. No. 2.2e+03; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
FT	SEQUENCE FROM N.A. STRAIN=BERKELEY;	RA	Qy 1 LLMWI 5 Db 3 LLRWL 7
FT	SEQUENCE FROM N.A. STRAIN=BERKELEY;	RA	RESULT 5 Q9G697 PRELIMINARY; ID Q9G697; PRT; 10 AA.
FT	SEQUENCE FROM N.A. STRAIN=BERKELEY;	RA	AC Q9G697; DT 01-MAR-2001 (TREMBLrel. 16, Created) DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update) DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
FT	SEQUENCE FROM N.A. STRAIN=BERKELEY;	RA	DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).

GN COI.
OS Chamaeleo dilepis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.
OC NCBITaxID=91908;
OX OS
RN [1]
RP SEQUENCE FROM N.A.
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
phylogenetics.";
RT Syst. Biol. 49:233-256(2000).
RL EMBL; AF128460; AAG00617.1; -.
KW Mitochondrion.
FT NON-TER 10 10 AA; 1319 MW; 5E218E2733640727 CRC64;
SQ SEQUENCE 10 AA; 1319 MW; 5E218E2733640727 CRC64;

Query Match 35.18; Score 20; DB 8; Length 10;
Best Local Similarity 60.08%; Pred. No. 2.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLMWI 5
Db 3 LLRWI 7

RESULT 6
Q9N1X1 PRELIMINARY; PRT; 10 AA.
ID Q9N1X1; AC Q9N1X1; DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ALCOHOL DEHYDROGENASE 3 (FRAGMENT).
GN ADH3.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus;
NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20082971; PubMed=10613847;
RA Caetano A.R., Shiue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA Bowling A.T., Murray J.D.;
RT "A comparative gene map of the horse (*Equus caballus*).";
RL Genome Res. 9:1239-1249(1999).
DR EMBL; AF134056; AAF31299.1; -.
FT NON-TER 1 1 AA; 1144 MW; C4EA25676B02D6DD CRC64;
FT NON-TER 10 10 AA; 1144 MW; C4EA25676B02D6DD CRC64;

Query Match 33.3%; Score 19; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.3e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WIT 6
Db 8 WWT 10

RESULT 7
Q9ESU5 PRELIMINARY; PRT; 10 AA.
ID Q9ESU5; AC Q9ESU5;

Query Match 33.3%; Score 19; DB 11; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.3e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LMWI 5
Db 1 MLWI 4

RESULT 8
Q9H326 PRELIMINARY; PRT;
ID Q9H326; AC Q9H326; DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE NAD+-DEPENDENT ISOCITRATE DEHYDROGENASE 3 ALPHA SUBUNIT
(FRAGMENT).
GN IDH3A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.-O., Koh H.-J., Jo S.-H., Son M.-K., Ruh T.-L.;
RT "Structural and functional characterization of the human NAD+-
dependent isocitrate dehydrogenase alpha subunit promoter.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157515; AAG43379.1; -.
FT NON-TER 9 9 AA; 960 MW; C91CB0437DC7687D CRC64;

Query Match 29.8%; Score 17; DB 4; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.6e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WITQ 7
Db 6 WISK 9

RESULT 9
Q38340 PRELIMINARY; PRT;
ID Q38340; AC Q38340; DT 01-NOV-1996 (TREMBLrel. 01, Created)
DR 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ORF PROTEIN (FRAGMENT).
GN [1]
OS Lactococcus phage 936.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TAXID=39838;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96084945; PubMed=7489923;
RA Waterfield N.R.; Lepage R.W.; Wilson P.W.; Wells J.M.;
RT "The isolation of lactococcal Promoters and their use in investigating
bacterial luciferase synthesis in Lactococcus lactis.";
RL Gene 165:9-15(1995).
DR EMBL; Z48181; CAA88226.1; -.
FT NON-TER 9 9 9
SQ SEQUENCE 9 AA; 1054 MW; 7098B2CEA6D3372B CRC64;

Query Match 29.8%; Score 17; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.6e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 10
ID Q48469 PRELIMINARY; PRT; 10 AA.
AC Q48469;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NITROGENASE (FRAGMENT).
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
RN NCBI_TAXID=573;
RP SEQUENCE FROM N.A.
RX MEDLINE=83246546; PubMed=6306580;
RA Shen S.C., Xue Z.T., Kong Q.T., Wu Q.L.;
RT "An open reading frame upstream from the nifH gene of Klebsiella
pneumoniae.";
RL Nucleic Acids Res. 11:4241-4250(1983).
DR EMBL; X01006; CAA25501.1; -.
FT NON-TER 10 10
SQ SEQUENCE 10 AA; 1173 MW; B130695DDEA6C406 CRC64;

Query Match 29.8%; Score 17; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.5e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 11
ID Q96QA7 PRELIMINARY; PRT; 10 AA.
AC Q96QA7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BA151A2.1 (CDC42 GUANINE EXCHANGE FACTOR (GEF) 9 (COLLYBISTIN, PEM-2,
ARHGEF9).
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC

OX NCBI_TAXID=52180;
RN [1]

OX NCBI_TAXID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Whitehead S.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL451106; CAC88408.1; -.
FT NON-TER 10 10
SQ SEQUENCE 10 AA; 1122 MW; 39925CB878640043 CRC64;

Query Match 29.8%; Score 17; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.5e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LMWI 5
Db 1 MQWI 4

RESULT 12
ID Q9TG98 PRELIMINARY; PRT; 10 AA.
AC Q9TG98;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN OS Shinisaurus crocodilurus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Shinisauridae;
OC Shinisaurus.
OX NCBI_TAXID=52224;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99343613; PubMed=10413621;
RA Macey J.R., Schulte J.A. III, Larson A., Tuneyev B.S., Orlov N.,
RA Papenfuss T.J.;
RA RT "Molecular phylogenetics, tRNA evolution, and historical biogeography
in anguid lizards and related taxonomic families.";
RT RL Mol. Phylogenet. Evol. 12:250-272(1999).
DR EMBL; AF085604; AAD51502.1; -.
KW Mitochondrion.
FT NON-TER 10 10
SQ SEQUENCE 10 AA; 1290 MW; 1CEE80C9D36411A0 CRC64;

Query Match 29.8%; Score 17; DB 8; Length 10;
Best Local Similarity 57.1%; Pred. No. 7.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 MWITQCF 9
Db 1 MTTRWF 7

RESULT 13
ID P92616 PRELIMINARY; PRT; 10 AA.
AC P92616;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update).
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN OS Cnemidophorus tigris.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Teiioidea;
OC Teiidae; Cnemidophorus.
OX NCBI_TAXID=52180;
RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE-97153826; PubMed-9000757;
 RA Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
 RT "Two novel gene orders and the role of light-strand replication in
 rearrangement of the vertebrate mitochondrial genome.";
 RL Mol. Biol. Evol. 14:91-104(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97153820; PubMed-9000751;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Replications slippage may cause parallel evolution in the secondary
 structures of mitochondrial transfer RNAs.";
 RL Mol. Biol. Evol. 14:30-39(1997).
 DR EMBL; U71332; AAB48274.1; - .
 KW Mitochondrion.
 FT NON_TER 10 10 MW; 1CEE80C9D36411A0 CRC64;
 SQ SEQUENCE 10 AA; 1290 MW; 297685A76AAB1734 CRC64;

Query Match 29.8%; Score 17; DB 8; Length 10;
 Best Local Similarity 57.1%; Pred. No. 7.5e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 MWIITQCF 9
 | || : 1
 Db 1 MTITRWF 7

RESULT 14
 Q94VJ4 PRELIMINARY; PRT; 8 AA.
 ID Q94VJ4;
 AC Q94VJ4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
 GN COI.
 OS Varanus bengalensis nebulosus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 OX NCBI_TAXID=169827;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA "Mitochondrial DNA evidence and evolution in varanoidea (Squamata).";
 RT Cladistics 17:0-0(2001);
 RL EMBL; AF407492; AAL10031.1; - .
 KW Mitochondrion.
 FT NON_TER 8 8 MW; E8B5B9C733640056 CRC64;
 SQ SEQUENCE 8 AA; 1053 MW; 28.1%; Score 16; DB 8; Length 8;
 Best Local Similarity 20.0%; Pred. No. 5.6e+05;
 Matches 1; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LLMWI 5
 | : 1;
 Db 1 MIRWL 5

RESULT 15
 Q9ET18 PRELIMINARY; PRT; 8 AA.
 ID Q9ET18;
 AC Q9ET18;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE NEUROPEPTIDE Y (FRAGMENT).
 OS Mus spretus (Western wild mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

PT Cancer antigen NY ESO1/CAG-3

XX Example 10; Page 42; 88pp; English.

This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see AAX58599). 30 Epitopes (see AAY05988-Y06017) were identified.

The present peptide (ranked 16) corresponds to amino acid residues 158-167 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, thyroid cancer, uterine cancer, cervical cancer, bladder cancer, kidney cancer, prostate, ovarian, pancreatic and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers.

XX Sequence 1.0 AA;

Query Match 100.0%; Score 57; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLMWITQCFL 10
Db 1 limwitqcf1 10

RESULT 2

AAY52434 standard; peptide; 10 AA.
XX AAY52434;

DT 15-FEB-2000 (first entry)

XX Human tumour antigen NY-ESO-1 peptide #7.
DE Cancer; tumour; antigen; MHC; major histocompatibility complex; Class I;
KW T-cell; cytotoxic; stimulation; proliferation; treatment;
KW diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW lymphoma.

XX OS Synthetic.
OS Homo sapiens.

XX PN WO9953938-A1.
XX PD 28-OCT-1999.

XX PR 24-MAR-1999; 99WO-US06875.
XX PR 17-APR-1998; 98US-0062422.
PR 02-OCT-1998; 98US-0165546.

XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
PI Gure A, Ritter G;
XX DR WPI; 2000-038483/03.

XX Novel peptides which bind to MHC class I and MHC class II molecules,
PT useful for therapeutic and diagnostic purposes -
XX Claim 55; Page 20; 49pp; English.

XX This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see AAX58599). 30 Epitopes (see AAY06018-47) were identified. The present peptide (ranked 15) corresponds to amino acid residues 159-167 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent

CC Peptides #4-#7 (AAY52431-Y52434) are peptides derived from the human CC tumour antigen, NY-ESO-1 (AAY52430) which contain the motif LLMWIT CC (AAY52441). These sequences can bind to MHC (major histocompatibility CC Class I HLA-A2 molecules, thereby stimulating proliferation of isolated CC cytotoxic T-cells. cDNA encoding NY-ESO-1 was initially isolated CC from an oesophagus squamous cell cancer cDNA library. Tissue CC localisation studies revealed it to be expressed at high levels CC in normal ovary and testis but not in normal colon, kidney, liver, CC brain, oesophagus and skin. It was expressed in certain tumours and CC tumour cell lines with some degree of frequency - these included CC melanoma specimens and cell lines, and breast and bladder cancer CC specimens, with expression in other tumour types being sporadic. CC These NY-ESO-1-derived peptides may be used in methods and CC compositions used for the treatment, diagnosis and prevention of CC cancers (such as melanoma, breast cancer, prostate cancer, lung CC cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, CC or lymphoma) and to stimulate the proliferation of T cells.

SQ Sequence 10 AA;

Query Match 100.0%; Score 57; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LLMWITQCFL 10
Db 1 limwitqcf1 10

RESULT 3

AAY06032 standard; peptide; 9 AA.
ID AAY06032
XX DT 16-AUG-1999 (first entry)
XX AC AAY06032;
XX DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA.

Homo sapiens.

XX OS Synthetic.
OS PN WO9918206-A2.
XX PD 15-APR-1999.

XX PR 08-OCT-1997;

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Rosenberg SA, Wang RF;

XX DR WPI; 1999-277270/23.

XX PT Cancer antigen NY ESO1/CAG-3
XX PS Example 10; Page 43; 88pp; English.

CC This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see AAX58599). 30 Epitopes (see AAY06018-47) were identified. The present peptide (ranked 15) corresponds to amino acid residues 159-167 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent

CC tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, carcinoma, cervical cancer, bladder cancer, kidney cancer and thyroid cancers.

XX Sequence 9 AA;

Query Match 93.0%; Score 53; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Gaps 0;

Qy 2 LMWITQCFL 10
| | | | | | |
Db 1 lmwitqcf 9

RESULT 4

AY06033

ID AY06033 standard; Peptide; 9 AA.

XX AC AAY06033;

XX DT 16-AUG-1999 (first entry)

XX DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.

XX KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human; leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer; metastasis; melanoma; adenocarcinoma; thymoma; colon cancer; uterine cancer; breast cancer; prostate cancer; ovarian cancer; cervical cancer; bladder cancer; kidney cancer; pancreatic cancer; liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy; vaccine; human leukocyte antigen; HLA; XX OS Homo sapiens.

XX PN WO9918206-A2.

XX PD 15-APR-1999.

XX PF 21-SEP-1998;

XX PR 08-OCT-1997;

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Rosenberg SA, Wang RF;

XX DR WPI; 1999-277270/23.

XX PT Cancer antigen NY ESO1/CAG-3

XX PS Example 10; Page 43; 88pp; English.

XX This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see AAX58599). 30 Epitopes (see AAY06018-47) were identified.

CC The present peptide (ranked 16) corresponds to amino acid residues 158-166 of CAG-1 ORF1 (see AAY05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, carcinoma, cervical cancer, bladder cancer, kidney cancer and thyroid cancers.

CC from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, uterine cancer, cervical cancer, kidney cancer, prostate, ovarian, pancreatic and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers.

XX SQ Sequence 9 AA;

Query Match 93.0%; Score 53; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
| | | | | | |
Db 1 lmwitqcf 9

RESULT 5

AY06033

ID AAY79756 standard; Peptide; 9 AA.

XX AC AAY79756

XX DT 10-MAY-2000 (first entry)

XX DE NY-ESO-1 derived peptide #12.

XX KW Cancer; SSX family; SSX-1; SSX-2; SSX-3; SSX-4; SSX-5; NY-ESO-1; HLA binding; human leukocyte antigen; cytolytic T cell; CTL; cytostatic; melanoma; synovial sarcoma.

XX OS Homo sapiens.

XX PN WO2000000824-A1.

XX PD 06-JAN-2000.

XX PF 25-JUN-1999; 99WO-US14493.

XX PR 26-JUN-1998; 98US-0105839.

XX PA (LUDWIG) LUDWIG INST CANCER RES.

XX PI Tureci O, Sahin U, Pfreundschuh M, Rammensee G, Stevanovic S; Chen Y, Gure A, Old LJ;

XX DR WPI; 2000-170933/15.

XX PT Determining the possible presence of breast, endometrial, colorectal, lung, bladder or head-neck cancer.

XX PS Example 13; Page 26; 40pp; English.

XX CC A method has been developed for determining the possible presence of a cancer, which is not melanoma or synovial sarcoma. The method comprises assaying a sample taken from the subject to determine the expression of an SSX gene, and determining the expression as a determination of the possible presence of cancer. Expression of SSX1 gene indicates possible presence of breast, endometrial, colorectal, lung, bladder or head-neck cancer. These cancers are also detected by SSX2 and SSX4 gene expression. SSX2 gene expression additionally indicates possible presence of lymphoma, renal cell cancer, glioma and prostate cancer. Expression of SSX4 gene also indicates possible presence of ovarian or stomach cancer. SSX5 gene expression indicates the same cancers as SSX1, except breast cancer. Determining expression of SSX gene can be used to monitor progress of melanoma or synovial sarcoma, which is not cancer. The SSX-derived peptide complex stimulates proliferation of cytolytic T cells. This is useful for treating cancer, especially melanoma. AAY78464 to AAY78468 represent specifically claimed HLA binding peptides for use in the method of the invention. AAZ88452 to AAZ88465 represent PCR primers used in the isolation of SSX genes in the exemplification of the present invention. AAY78469 to AAY78500, and AAY79684 to AAY79762

CC represent peptides derived from SSX proteins or NY-ESO-1, which are used
 CC in the exemplification of the present invention.

XX Sequence 9 AA;

Query Match 93.0%; Score 53; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 LMWITQCF1 10
 Db 1 1mwitqcf1 9

RESULT 6

AAG67170 ID AAG67170 standard; peptide; 9 AA.

XX AC AAG67170;

XX DT 13-NOV-2001 (first entry)

XX DE Cancer testis tumour antigen NY-ESO-1 derived peptide.

XX KW Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;

CC HLA; HLA binding peptide; major histocompatibility complex; MHC;

CC tumour; cancer; testis tumour.

XX OS Homo sapiens.

XX PN WO200162917-A1.

XX PD 30-AUG-2001.

XX PF 22-JAN-2001; 2001WO-US02126.

XX PR 22-FEB-2000; 2000US-0510635.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Lethe B, Boon-Falleur T;

XX DR WPI; 2001-550091/61.

XX PT Genomic sequences of tumour associated antigen NY-ESO-1 (LAGE-2) useful

PT for diagnosing testicular tumours -

XX PS Example 13; Page 26; 50pp; English.

XX XX AAG67169-AAG67206 represent peptides which are derived from cancer

CC testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptides

CC bind to human leukocyte antigens (HLAs). NY-ESO-1 is a molecule that

CC is processed to at least one human leukocyte antigen (HLA) binding

CC peptide, which binds to Class I and Class II major histocompatibility

CC complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis,

CC but not normal colon, kidney, liver or brain tissue. The presence or

CC level of expression of NY-ESO-1 may be assayed for the diagnosis of

CC cancer, especially testis tumours.

XX SQ Sequence 9 AA;

XX PT Genomic sequences of tumour associated antigen NY-ESO-1 (LAGE-2) useful

PT for diagnosing testicular tumours -

XX PS Example 13; Page 26; 50pp; English.

XX XX AAG67169-AAG67206 represent peptides which are derived from cancer

CC testis tumour antigen NY-ESO-1 (also called LAGE-2). The peptides

CC bind to human leukocyte antigens (HLAs). NY-ESO-1 is a molecule that

CC is processed to at least one human leukocyte antigen (HLA) binding

CC peptide, which binds to Class I and Class II major histocompatibility

CC complex (MHC). NY-ESO-1 is expressed in tumour mRNA and in testis,

CC but not normal colon, kidney, liver or brain tissue. The presence or

CC level of expression of NY-ESO-1 may be assayed for the diagnosis of

CC cancer, especially testis tumours.

XX SQ Sequence 9 AA;

XX Query Match 93.0%; Score 53; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9

Db 1 1lmwitqcf 9

RESULT 7

Query Match 93.0%; Score 53; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9

Db 1 1lmwitqcf 9

RESULT 8

Query Match 93.0%; Score 53; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9

Db 1 1lmwitqcf 9

RESULT 9

Query Match 93.0%; Score 53; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9

Db 1 1lmwitqcf 9

RESULT 10

Query Match 93.0%; Score 53; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9

Db 1 1lmwitqcf 9

RESULT 11

Query Match 93.0%; Score 53; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9

Db 1 1lmwitqcf 9

RESULT 12

Query Match 93.0%; Score 53; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9

Db 1 1lmwitqcf 9

RESULT 13

Query Match 93.0%; Score 53; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9

Db 1 1lmwitqcf 9

RESULT 14

Query Match 93.0%; Score 53; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9

Db 1 1lmwitqcf 9

RESULT 15

Query Match 93.0%; Score 53; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9

Db 1 1lmwitqcf 9

RESULT 16

Query Match 93.0%; Score 53; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9

Db 1 1lmwitqcf 9

RESULT 17

Query Match 93.0%; Score 53; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9

Db 1 1lmwitqcf 9

RESULT 18

Query Match 93.0%; Score 53; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9

Db 1 1lmwitqcf 9

RESULT 19

Query Match 93.0%; Score 53; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9

Db 1 1lmwitqcf 9

RESULT 20

Query Match 93.0%; Score 53; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9

Db 1 1lmwitqcf 9

RESULT 21

Query Match 93.0%; Score 53; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9

Db 1 1lmwitqcf 9

RESULT 22

Query Match 93.0%; Score 53; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.4e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF 9

Db 1 1lmwitqcf 9

RESULT 23

Query Match 93.0%; Score 53; DB 22; Length 9;</

XX XX Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
 PD PI XX DR WPI; 2001-182822/18.

XX PR 23-JUL-1999; 99US-0359503.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (CORR) CORNELL RES FOUND INC.

PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;
 XX DR WPI; 2001-182822/18.

XX PT Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a patient -

XX PS Example 14; Page 24; 50pp; English.

XX CC The present sequence is given in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for determining whether a cancerous condition is progressing, regressing or remaining stable, in particular in patients receiving treatment for a melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder carcinoma.

XX SQ Sequence 9 AA;

Query Match 93.0%; Score 53; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LLMWITQCF 10
 |||||
 1 lmwitqcf 9

Db

XX RESULT 10
 AAY06006
 ID AAY06006 standard; Peptide; 10 AA.
 XX AC AAY06006,
 XX DT 16-AUG-1999 (first entry)
 XX DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
 XX KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
 KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
 KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
 KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
 KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
 KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
 KW vaccine; human leukocyte antigen; HLA.
 XX OS Homo sapiens.
 XX PN WO9918206-A2.
 ID AAB69903
 XX AAB69903 standard; Peptide; 9 AA.
 AC AAB69903;
 XX DT 27-APR-2001 (first entry)
 XX DE Human NY-ESO-1 HLA binding motif #3.
 XX KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
 KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
 KW non-small cell lung carcinoma; tumour status determination.
 XX OS Homo sapiens.
 XX PN WO200107917-A1.
 XX PD 01-FEB-2001.
 XX PR 14-JUL-2000; 2000WO-US19220.
 XX PR 23-JUL-1999; 99US-0359503.
 PA (LUDW-) LUDWIG INST CANCER RES.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (CORR) CORNELL RES FOUND INC.

XX PT Cancer antigen NY ESO1/CAG-3
 XX PS Example 10; Page 42; 88pp; English.

This peptide was identified as an HLA peptide motif following a screen for epitopes from the coding region of human ESO-1/CAG-3 ORF1 (see AAX58599). 30 Epitopes (ranked 19) corresponds to amino acid residues 157-166 of CAG-1 ORF1 (see AY05965). CAG-1 is a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides (see AAY05967-87) derived from CAG-3, portions of CAG-3 and their variants, are useful as cancer vaccines. A claimed method of preventing or inhibiting cancer involves administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers.

XX SQ Sequence 10 AA;

Query Match 93.0%; Score 53; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
||||| |||||
Db 2 llmwitqcf 10

RESULT 11

AAB85307 ID AAB85307 standard; peptide; 10 AA.
XX AC AAB85307;

DE HLA-A2 binding NY-ESO-1 peptide (residues 157-166).

XX DT 17-SEP-2001 (first entry)
XX KW NY-ESO-1; human leukocyte antigen; HLA; lysis; cytolytic T cell; CTL;
KW HLA-A2; T-cell sorter; tumor; immune tetrramer.
XX OS Homo sapiens.
XX PN WO200136453-A2.
XX PD 25-MAY-2001.

XX PF 08-NOV-2000; 2000WO-US42010.
XX PR 15-NOV-1999; 99US-0440621.
PR 25-FEB-2000; 2000US-0514036.
PR 29-SEP-2000; 2000US-0676005.

XX PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYOX-) UNIV OXFORD.
XX PI Valmori D, Cerottini J, Romero P, Cerundolo V;
XX DR 2001-451454/48.

XX PS Novel isolated NY-ESO-1 nonapeptide useful for determining if a cell presents a NY-ESO-1 peptide derivative which binds to human leukocyte antigen-A2 molecule on its surface, binds to human leukocyte antigen molecules and provokes lysis by cytolytic T cells -
XX Example 11; Page 11; 38pp; English.
XX PT The invention provides NY-ESO-1 peptide derivatives which bind to human leukocyte antigen (HLA) molecules and provokes lysis by cytolytic T cells (CTLs). The NY-ESO-1 nonapeptide is of formula SLLMWITQCF, where X is an amino acid having an uncharged polar side chain. The NY-ESO-1 peptide CC monitor the efficacy of a therapeutic regime.

CC derivatives are useful for determining if a cell presents an HLA-A2 molecule on its surface, by contacting a sample containing the cell with the peptide or its derivative, and determining binding between them, where the binding is indicative of HLA-A2 on the surface of the cell. The NY-ESO-1 peptides and analogues are useful therapeutically, for administration to a patient who is HLA-A2 positive and expresses NY-ESO-1 in connection with the pathology, as well as diagnostically, i.e. to determine if HLA-A2 positive cells are present, or if relevant CTUs are present. They are also useful for determining the presence of CTUs in a sample. The peptides are useful as T-cell sorters, when incorporated into immune tetramers. The present sequence represents a NY-ESO-1 peptide that can bind to HLA-A2 molecule.

CC Query Match 93.0%; Score 53; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQCF 9
||||| |||||
ID AAW62586 standard; Peptide; 9 AA.
XX
AC AAW62586;
XX DT 17-SEP-1998 (first entry)
XX DE Cancer associated antigen peptide.
XX KW Cancer associated antigen; NY-ESO-1; regression; progression; onset; cancer; treatment; diagnosis.
XX OS Synthetic.
OS Homo sapiens.
XX PN WO9814464-A1.
XX PD 09-APR-1998.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PF 15-SEP-1997; 97WO-US16335.
XX PR 03-OCT-1996; 96US-0725182.
XX DR WPI; 1998-286417/25.
XX PT New isolated cancer associated antigen - is used to develop products for the diagnosis and treatment of cancers and for monitoring cancer therapy
XX PS Claim 33; Page 17; 49pp; English.

CC Peptides AAW62585-87 are derived from cancer associated antigen NY-ESO-1, and are stimulators of cytotoxic T-cells. The specification describes a method for determining regression, progression of onset of a cancerous condition, comprising monitoring a sample from a patient with the cancerous condition for a parameter selected from NY-ESO-1 protein, a peptide derived from NY-ESO-1 protein and cytolytic T cells specific for the peptide and an MHC molecule with which it non-covalently complexes. Methods for the treatment of a cancerous condition are also described. The NY-ESO-1 protein and peptides derived from it can be used for diagnosis and treatment of cancers and to monitor the efficacy of a therapeutic regime.

XX	SQ	Sequence	9 AA;	RESULT 14
		Query Match	82.5%; Score 47; DB 19; Length 9;	AAB08703
		Best Local Similarity	100.0%; Pred. No. 6.4e+05;	ID AAB08703 standard; Peptide; 9 AA.
		Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX
Qy	1	LLMWITQC 8		XX
				AC
Db	2	11mwitqc 9		XX
				DT 02-JAN-2001 (first entry)
				XX
				DE Antigenic peptide from tumour rejection antigen NY-ESO-1.
				XX
				KW EPHA3; HLA class II-binding peptide; human leukocyte antigen; antigen; CD4+ T lymphocyte; tumour associated gene; vaccine.
				XX
				OS Homo sapiens.
				XX
				PN WO2000050589-A1.
				XX
				PD 31-AUG-2000.
				XX
				PF 18-FEB-2000; 2000WO-US04326.
				XX
				PR 22-FEB-1999; 99US-0121170.
				XX
				PR 08-OCT-1999; 99US-0158566.
				XX
				(LUDW-) LUDWIG INST CANCER RES.
				PA
				XX
				PI Chiari R, Coulie P, Boon-Falleur T;
				XX
				WPI; 2000-572089/53.
				XX
				DR
				XX
				PT Novel tyrosine kinase receptor, EphA3 human leukocyte antigen (HLA) class II binding peptide and nucleic acid encoding the receptor, useful for diagnosing and treating conditions characterized by expression of EphA3 gene -
				XX
				PT Disclosure; Page 36; 107pp; English.
				XX
				CC AAB08668-B08704 represent antigenic peptides characteristic of tumours.
				CC The peptides may be combined in vaccines with a human EphA3 HLA (human leukocyte antigen) class II-binding peptide. EphA3 antigens, when presented by an antigen presenting cell having a HLA class II molecule, effectively induce activation and proliferation of CD4+ T lymphocytes.
				CC EphA3 is a tumour associated gene. EphA3 HLA binding peptides are used for selectively enriching a population of T lymphocytes. The peptides are also used for diagnosing a disorder characterized by EphA3 or EphA3 HLA binding peptide expression. The peptides are also used to treat a disorder characterized by EphA3 expression. The EphA3 binding peptides are useful in producing vaccines and antibody.
				XX
				PS Sequence 9 AA;
				XX
				PA (LUDW-) LUDWIG INST CANCER RES.
				PA (UYVR-) UNIV VRIJE BRUSSEL.
				XX
				PI Boon-Falleur T, Chaux P, Corthals J, Heirman C;
				PI Luiten R, Stroobant V, Thielemans K, Van Der Bruggen P;
				XX
				DR WPI; 1999-244031/20.
				XX
				PT Isolated peptides that bind to human leucocyte antigen class II molecules
				XX
				PT Disclosure; Page 29; 88pp; English.
				XX
				CC The present sequence represents an exemplary tumour associated peptide antigen. The specification describes a MAGE-3 tumour associated gene.
				CC Peptides (AY01721-25) that bind human leucocyte antigen (HLA) Class II molecules can be derived from the MAGE-3 protein. These peptides and
				CC autologous CD4+ cells that bind to a complex of MAGE-3 peptide and HLA Class II, are used to treat MAGE-3 related diseases, particularly cancers (e.g. melanoma, osteosarcoma, leukemia and various forms of carcinoma). The peptides are also used to produce specific antibodies. Detection of the peptides, e.g. in binding assays, particularly with antibodies, is used for diagnosis of such diseases.
				XX
				PS Sequence 9 AA;
				XX
				Query Match 82.5%; Score 47; DB 21; Length 9;
				Best Local Similarity 100.0%; Pred. No. 6.4e+05;
				Mismatches 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	LLMWITQC 8		XX
				AC
Db	2	11mwitqc 9		XX
				DT 22-DEC-2000 (first entry)
				XX
				DE NY-ESO-1 peptide epitope, SEQ ID NO:2.
				XX
				KW NY-ESO-1; epitope; CTL response; cytotoxic T lymphocyte; vaccine;

KW immunogenic; adjuvant coadministration; microbial infection;
 KW tuberculosis; HIV; hepatitis B virus; hepatitis C virus; cancer.
 XX Unidentified.

OS WO200048630-A1.

XX 24-AUG-2000.

XX PF 17-FEB-2000; 2000WO-AU00110.

XX PR 17-FEB-1999; 99AU-0008735.

XX PR 27-JUL-1999; 99AU-0001861.

XX PA (CSLC-) CSL LTD.

XX PI Cox JC, Drane DP;

XX DR; 2000-571930/53.

XX PT Immunogenic complexes comprising negatively charged organic carrier
 PT adjuvants and positively charged antigens for use as vaccines against
 PT microbial infection and cancer

XX PS Example 4; Fig 5c; 111pp; English.

XX The invention relates to a novel immunogenic complex comprising a
 CC charged organic carrier and a charged antigen which are
 CC electrostatically associated. The complex induces a cytotoxic T
 CC lymphocyte (CTL) response. The complex and/or vaccine can be used to
 CC treat a disease in a mammal, where the complex/vaccine elicits, induces
 CC or otherwise facilitates an immune response which inhibits, halts, delays
 CC or prevents the onset or progression of the disease condition. In
 CC particular, the disease is a condition resulting from a microbial
 CC infection or cancer. Microbial infections which may be treated using the
 CC immunogenic complex include human immunodeficiency virus (HIV), hepatitis
 CC B, hepatitis C, tuberculosis or a parasitic condition, and cancers which
 CC may be treated include melanoma, prostate cancer or breast cancer. The
 CC complexes and vaccines simultaneously co-deliver antigen and adjuvant to
 CC the same antigen presenting cell, which is often essential for induction
 CC of appropriate immune responses. Sequences AAB22790-B22791 represent
 CC peptide epitopes of the positively charged protein NY-ESO-1 used in an
 CC exemplification of the invention.

XX SO Sequence 9 AA;

Query Match 82.5%; Score 47; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
 |||||||
 Db 2 llmwitqc 9

Search completed: July 16, 2002, 08:01:30
 Job time: 783 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 08:00:52 ; Search time 73.89 Seconds

(without alignments)
47.636 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCEL 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 316561

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

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8 53 93.0 9 19 US-09-529-206A-71 Sequence 71, Appl
9 53 93.0 9 19 US-09-529-206A-72 Sequence 72, Appl
10 53 93.0 9 19 US-09-529-206B-71 Sequence 71, Appl
11 53 93.0 9 19 US-09-529-206B-72 Sequence 72, Appl
12 53 93.0 9 22 US-09-833-039-123 Sequence 123, Appl
13 53 93.0 10 19 US-09-529-206-95 Sequence 95, Appl
14 53 93.0 10 19 US-09-529-206A-95 Sequence 95, Appl
15 53 93.0 10 19 US-09-529-206B-95 Sequence 95, Appl
16 53 93.0 10 20 US-09-676-005B-11 Sequence 11, Appl
17 47 82.5 9 1 PCT-US00-04326-43 Sequence 43, Appl
18 47 82.5 9 1 PCT-US99-06875-5 Sequence 5, Appl
19 47 82.5 9 15 US-06-670-456A-1 Sequence 1, Appl
20 47 82.5 9 15 US-09-165-546A-5 Sequence 5, Appl
21 47 82.5 9 17 US-09-336-091-42 Sequence 42, Appl
22 47 82.5 9 17 US-09-396-315-80 Sequence 80, Appl
23 47 82.5 9 18 US-09-408-036B-5 Sequence 5, Appl
24 47 82.5 9 18 US-09-440-621-2 Sequence 2, Appl
25 47 82.5 9 19 US-09-510-635A-5 Sequence 5, Appl
26 47 82.5 9 19 US-09-574-749-34 Sequence 34, Appl
27 47 82.5 9 20 US-09-676-005B-2 Sequence 2, Appl
28 47 82.5 9 20 US-09-692-401-44 Sequence 44, Appl
29 47 82.5 9 20 US-09-697-884-80 Sequence 80, Appl
30 47 82.5 9 21 US-09-705-160-43 Sequence 43, Appl
31 47 82.5 9 21 US-09-751-798-5 Sequence 5, Appl
32 47 82.5 9 21 US-09-766-889A-51 Sequence 51, Appl
33 47 82.5 9 23 US-09-913-756-43 Sequence 43, Appl
34 47 82.5 9 24 US-10-023-182-5 Sequence 5, Appl
35 47 82.5 9 24 US-10-080-013-24 Sequence 24, Appl
36 47 82.5 9 26 US-60-336-968-12 Sequence 12, Appl
37 47 82.5 10 20 US-09-676-005B-13 Sequence 13, Appl
38 47 82.5 10 20 US-09-529-206-68 Sequence 14, Appl
39 44 77.2 9 19 US-09-529-206A-68 Sequence 68, Appl
40 44 77.2 9 19 US-09-529-206B-68 Sequence 68, Appl
41 44 77.2 9 19 US-09-529-206-94 Sequence 94, Appl
42 44 77.2 10 19 US-09-529-206B-94 Sequence 94, Appl
43 44 77.2 10 19 US-09-529-206A-94 Sequence 94, Appl
44 44 77.2 10 19 US-09-529-206B-94 Sequence 94, Appl
45 44 77.2 10 20 US-09-676-005B-17 Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-165-546A-7
; Sequence 7, Application US/09165546A

GENERAL INFORMATION:

APPLICANT: Knuth, Alexander; Jager, Elke; Chen, Yao,
Canlan, Matt; Gure, Ali; Old, Lloyd, Ritter, Gerd

TITLE OF INVENTION: ISOLATED PEPTIDES CORRESPONDING TO
AMINO ACID SEQUENCES OF NY-ESO-1, WHICH BIND TO
MHC CLASS I AND MHC CLASS II MOLECULES, AND
USES THEREOF

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: FULBRIGHT & JAWORSKI LLP
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10158

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,546A
FILING DATE: 02-Oct-1998
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998

SUMMARIES

Result No.	Query	Match	Length	DB	ID	Description
1	57	100.0	10	15	US-09-165-546A-7	Sequence 7, Appl
2	57	100.0	10	19	US-09-529-206-92	Sequence 92, Appl
3	57	100.0	10	19	US-09-529-206A-92	Sequence 92, Appl
4	57	100.0	10	19	US-09-529-206B-92	Sequence 92, Appl
5	53	93.0	9	18	US-09-409-455A-123	Sequence 123, Appl
6	53	93.0	9	19	US-09-529-206-71	Sequence 71, Appl
7	53	93.0	9	19	US-09-529-206-72	Sequence 72, Appl

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

APPLICATION NUMBER: 08/937,263
 FILING DATE: September 15, 1997
 APPLICATION NUMBER: US 08/752,182
 FILING DATE: 03-October-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, Norman D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5466.3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-09-165-546A-7

Query Match 100.0%; Score 57; DB 15; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLMWITQCFL 10
 Db 1 LLMWITQCFL 10

RESULT 2
 US-09-529-206-92
 Sequence 92, Application US/09529206
 GENERAL INFORMATION:
 APPLICANT: The Government of the United States of America as
 TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
 TITLE OF INVENTION: Encoding Same
 FILE REFERENCE: 20264269PC
 CURRENT APPLICATION NUMBER: US/09/529,206
 CURRENT FILING DATE: 2000-06-13
 PRIOR APPLICATION NUMBER: US60/061,428
 PRIOR FILING DATE: 1997-10-08
 NUMBER OF SEQ ID NOS: 106
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 92
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-529-206-92

Query Match 100.0%; Score 57; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLMWITQCFL 10
 Db 1 LLMWITQCFL 10

Query Match 100.0%; Score 57; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLMWITQCFL 10
 Db 1 LLMWITQCFL 10

RESULT 3
 US-09-529-206A-92
 Sequence 92, Application US/09529206A
 GENERAL INFORMATION:
 APPLICANT: Wang Rong, Fu
 APPLICANT: Rosenberg, Steven
 TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
 TITLE OF INVENTION: Encoding Same
 FILE REFERENCE: 20264269US1
 CURRENT APPLICATION NUMBER: US/09/529,206A
 CURRENT FILING DATE: 2000-06-13
 PRIOR APPLICATION NUMBER: PCT/US98/19609
 PRIOR FILING DATE: 1998-09-21
 NUMBER OF SEQ ID NOS: 129
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 92
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-529-206B-92

Query Match 100.0%; Score 57; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLMWITQCFL 10
 Db 1 LLMWITQCFL 10

Query Match 100.0%; Score 57; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLMWITQCFL 10
 Db 1 LLMWITQCFL 10

Query Match 100.0%; Score 57; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLMWITQCFL 10
 Db 1 LLMWITQCFL 10

RESULT 4
 US-09-529-206B-92
 Sequence 92, Application US/09529206B
 GENERAL INFORMATION:
 APPLICANT: Wang Rong, Fu
 APPLICANT: Rosenberg, Steven
 TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
 TITLE OF INVENTION: Encoding Same
 FILE REFERENCE: 20264269US1
 CURRENT APPLICATION NUMBER: US/09/529,206B
 CURRENT FILING DATE: 2000-06-13
 PRIOR APPLICATION NUMBER: PCT/US98/19609
 PRIOR FILING DATE: 1998-09-21
 NUMBER OF SEQ ID NOS: 129
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 92
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-529-206B-92

Query Match 100.0%; Score 57; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLMWITQCFL 10
 Db 1 LLMWITQCFL 10

Query Match 100.0%; Score 57; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLMWITQCFL 10
 Db 1 LLMWITQCFL 10

Query Match 100.0%; Score 57; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLMWITQCFL 10
 Db 1 LLMWITQCFL 10

Query Match 100.0%; Score 57; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLMWITQCFL 10
 Db 1 LLMWITQCFL 10

RESULT 5
 US-09-409-455A-123
 Sequence 123, Application US/09409455A
 GENERAL INFORMATION:
 APPLICANT: Tureci, Ozlem
 APPLICANT: Sahin, Ugur
 APPLICANT: Pfreundschnuh, Michael
 TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
 FILE REFERENCE: LUD 5622
 CURRENT APPLICATION NUMBER: US/09/409,455A
 CURRENT FILING DATE: 1999-09-30
 PRIOR APPLICATION NUMBER: US 09/344,040
 PRIOR FILING DATE: 1999-06-25
 PRIOR APPLICATION NUMBER: US 09/105,839
 PRIOR FILING DATE: 1998-06-26
 PRIOR APPLICATION NUMBER: US 08/851,130
 PRIOR FILING DATE: 1997-05-05
 NUMBER OF SEQ ID NOS: 129
 SEQ ID NO: 123
 LENGTH: 9
 TYPE: PRT

```

; ORGANISM: Homo sapiens
; US-09-409-455A-123
RESULT 8
US-09-529-206A-71
; Sequence 71, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; SEQ ID NO: 71
; US-09-529-206A-71

Query Match 93.0%; Score 53; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LMWITQCFL 10
Db 1 LMWITQCFL 9

RESULT 6
US-09-529-206-71
; Sequence 71, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 71
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-529-206-71

Query Match 93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LMWITQCFL 10
Db 1 LMWITQCFL 9

RESULT 9
US-09-529-206A-72
; Sequence 72, Application US/09529206A
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206A
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-529-206A-72

Query Match 93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LMWITQCFL 10
Db 1 LMWITQCFL 9

RESULT 7
US-09-529-206-72
; Sequence 72, Application US/09529206
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America as
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269PC
; CURRENT APPLICATION NUMBER: US/09/529,206
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 72
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-529-206-72

Query Match 93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 9
Db 1 LLMWITQCFL 9

RESULT 10
US-09-529-206B-71
; Sequence 71, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-529-206B-71

Query Match 93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCFL 9
Db 1 LLMWITQCFL 9

```

```

; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIORITY APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 71
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-529-206B-71

Query Match 93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LMWITQCFL 10
Db 1 LMWITQCFL 9

RESULT 11
US-09-529-206B-72
; Sequence 72, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 72
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-529-206B-72

Query Match 93.0%; Score 53; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMWITQCFL 9
Db 1 LMWITQCFL 9

RESULT 12
US-09-833-039-123
; Sequence 123, Application US/09833039
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 09/344,040
; ORGANISM: Homo sapiens
; US-09-833-039-123

```

US-09-529-206A-95

```

Query Match      93.0%;  Score 53;  DB 19;  Length 10;
Best Local Similarity 100.0%;  Pred. No. 0.41;
Matches 9;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
QY      1 LLMWITQCF 9
        |||||||||
Db      2 LLMWITQCF 10

```

```

RESULT 15
US-09-529-206B-95
; Sequence 95, Application US/09529206B
; GENERAL INFORMATION:
; APPLICANT: Wang Rong, Fu
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: Novel Human Cancer Antigen NY ESO-1/CAG-3 and Gene
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 20264269US1
; CURRENT APPLICATION NUMBER: US/09/529,206B
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: PCT/US98/19609
; PRIOR FILING DATE: 1998-09-21
; PRIOR APPLICATION NUMBER: US60/061,428
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-206B-95

```

```

Query Match      93.0%;  Score 53;  DB 19;  Length 10;
Best Local Similarity 100.0%;  Pred. No. 0.41;
Matches 9;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
QY      1 LLMWITQCF 9
        |||||||||
Db      2 LLMWITQCF 10

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Search completed: July 16, 2002, 08:04:54
Job time: 242 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 16, 2002, 08:00:02 ; Search time 16.99 Seconds
 (without alignments)
 65.466 Million cell updates/sec

Title: US-09-165-546A-7
 Perfect score: 57
 Sequence: 1 LLMWITQCF1L 10

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 344541 seqs, 111227333 residues

Total number of hits satisfying chosen parameters: 37342

Minimum DB seq length: 0
 Maximum DB seq length: 10

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Pending_Patents_AA_New:*

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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

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7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	53	93.0	9	5	US-09-344-040C-123	Sequence 123, App
2	53	93.0	9	6	US-10-177-277-123	Sequence 123, App
3	47	82.5	9	1	PCT-US02-05748-24	Sequence 24, App
4	47	82.5	9	5	US-09-344-040C-131	Sequence 131, App
5	47	82.5	9	5	US-09-670-456A-1	Sequence 1, App
6	47	82.5	9	5	US-09-574-749B-34	Sequence 34, App
7	47	82.5	9	6	US-10-117-937-197	Sequence 197, App
8	47	82.5	9	6	US-10-177-277-131	Sequence 131, App
9	44	77.2	9	6	US-10-117-937-196	Sequence 196, App
10	38	66.7	9	1	PCT-US02-05748-25	Sequence 25, App
11	33	57.9	9	1	PCT-US02-05748-26	Sequence 26, App
12	33	57.9	9	5	US-09-344-040C-122	Sequence 122, App
13	33	57.9	9	5	US-09-344-040C-132	Sequence 132, App
14	33	57.9	9	5	US-09-574-749B-35	Sequence 35, App
15	33	57.9	9	6	US-10-177-277-132	Sequence 122, App
16	33	57.9	9	6	US-09-344-040C-129	Sequence 129, App
17	33	57.9	10	5	US-09-344-040C-129	Sequence 203, App
18	33	57.9	10	6	US-10-117-937-203	Sequence 129, App
19	33	57.9	10	6	US-10-117-277-129	Sequence 638, App
20	30	52.6	9	5	US-09-595-334C-638	Sequence 638, App
21	30	52.6	9	5	US-09-602-016C-638	Sequence 638, App
22	30	52.6	9	5	US-09-570-582C-797	Sequence 797, App
23	30	52.6	9	5	US-09-602-152C-638	Sequence 638, App
24	30	52.6	9	5	US-09-621-630B-638	Sequence 3789, App
25	30	52.6	10	6	US-10-105-299-3789	Sequence 202, App
26	29	50.9	9	6	US-10-117-937-202	Sequence 202, App

ALIGNMENTS

RESULT 1
 US-09-344-040C-123
 ; Sequence 123, Application US/09344040C
 ; GENERAL INFORMATION:
 ; APPLICANT: Tureci, Ozlem
 ; APPLICANT: Sahin, Ugur
 ; APPLICANT: Pfreundschuh, Michael
 ; APPLICANT: Ramensee, Hans Georg
 ; APPLICANT: Stevanovic, Stefan
 ; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Deter
 ; TITLE OF INVENTION: Expression Of an SSX Gene, Peptides Derived From Said SSX Gen
 ; TITLE OF INVENTION: Gene, and Uses Thereof
 ; FILE REFERENCE: LUD 5556.1
 ; CURRENT APPLICATION NUMBER: US/09-344-040C
 ; CURRENT FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: US 09/105,839
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 08/851,130
 ; PRIOR FILING DATE: 1997-05-05
 ; NUMBER OF SEQ ID NOS: 132
 ; SEQ ID NO 123
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-344-040C-123

Query Match 93.0%; Score 53; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LMWITQCFL 10
 Db 1 LMWITQCFL 9

RESULT 2
 US-10-177-277-123
 ; Sequence 123, Application US/10177277
 ; GENERAL INFORMATION:
 ; APPLICANT: Tureci, Ozlem
 ; APPLICANT: Sahin, Ugur
 ; APPLICANT: Pfreundschuh, Michael
 ; APPLICANT: Ramensee, Hans Georg
 ; APPLICANT: Stevanovic, Stefan
 ; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Deter
 ; TITLE OF INVENTION: Expression Of an SSX Gene, Peptides Derived From Said SSX Gen
 ; TITLE OF INVENTION: Gene, and Uses Thereof
 ; FILE REFERENCE: LUD 5556.1

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; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-177-277-123

Query Match 93.0%; Score 53; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LMWITQCFL 10
| | | | | | | |
Db 1 LMWITQCFL 9

RESULT 3
PCT-US02-05748-24
; Sequence 24, Application PC/TUSS0205748
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Leturcq, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Marja
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: PCT/US02/05748
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US02-05748-24

Query Match 82.5%; Score 47; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQC 8
| | | | | | | |
Db 2 LLMWITQC 9

RESULT 4
US-09-344-040C-131
; Sequence 131, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determination of Expression of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof
; FILE REFERENCE: LUD 555.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839

Query Match 82.5%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQC 8
| | | | | | | |
Db 2 LLMWITQC 9

RESULT 5
US-09-670-456A-1
; Sequence 1, Application US/09670456A
; GENERAL INFORMATION:
; LUD-5668-PCT
; APPLICANT: Gnijatic, Sacha
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA-C MOLECULES AND USES THEREOF
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: LUD 5668
; CURRENT APPLICATION NUMBER: US/09/670,456A
; CURRENT FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 5
SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-670-456A-1

Query Match 82.5%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQC 8
| | | | | | | |
Db 2 LLMWITQC 9

RESULT 6
US-09-574-749B-34
; Sequence 34, Application US/09574749B
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADDEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; CURRENT APPLICATION NUMBER: US/09/574,749B
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 9

Query Match 82.5%; Score 47; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQC 8
| | | | | | | |
Db 2 LLMWITQC 9

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```

; TYPE: PRT ; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
US-09-574-749B-34

Query Match 82.5%; Score 47; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Organism: Homo sapiens
US-10-177-277-131

Qy 1 LLMWITQC 8
Db 2 LLMWITQC 9

RESULT 7
US-10-117-937-197
; Sequence 197, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 197
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-197

Query Match 82.5%; Score 47; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Organism: Homo sapiens
US-10-117-937-196

Qy 1 LLMWITQC 8
Db 2 LLMWITQC 9

RESULT 9
US-10-117-937-196
; Sequence 196, Application US/10117937
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 196
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-196

Query Match 82.5%; Score 47; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Organism: Homo sapiens
US-10-117-937-196

Qy 1 LLMWITQC 8
Db 2 LLMWITQC 9

RESULT 10
PCT-US02-05748-25
; Sequence 25, Application PC/TUS0205748
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Leturcq, Didier
; APPLICANT: Degrav, Juli
; APPLICANT: Heiskala, Maria
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORP-1557
; CURRENT APPLICATION NUMBER: PCT/US02/05748
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 25
; LENGTH: 9

Query Match 77.2%; Score 44; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Organism: Homo sapiens
US-10-117-937-196

Qy 4 WITQCFL 10
Db 1 WITQCFL 7

RESULT 8
US-10-177-277-131
; Sequence 131, Application US/10177277
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining Expression of an SSX Gene, Peptides Derived From Said SSX Gene and Uses Thereof
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 25
; LENGTH: 9

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; TYPE: PRT ; ORGANISM: Homo sapiens
; PCT-US02-05748-25

Query Match      66.7%; Score 38; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 LLMWITQ 7
    ||||| Db  2 LLMWITQ 8

RESULT 11
PCT-US02-05748-26
; Sequence 26, Application PC/TUS0205748
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Leturcq, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Marja
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: PCT/US02/05748
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US02-05748-26

Query Match      57.9%; Score 33; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 LLMWIT 6
    ||||| Db  4 LLMWIT 9

RESULT 12
US-09-344-040C-122
; Sequence 122, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determination of an SSX Gene, Peptides Derived From Said SSX Gen
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gen
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-344-040C-122

Query Match      57.9%; Score 33; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 LLMWIT 6
    ||||| Db  4 LLMWIT 9

RESULT 13
US-09-344-040C-132
; Sequence 132, Application US/09344040C
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Deter
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gen
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-344-040C-132

Query Match      57.9%; Score 33; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 LLMWIT 6
    ||||| Db  4 LLMWIT 9

RESULT 14
US-09-574-749B-35
; Sequence 35, Application US/09574749B
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADDEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; TITLE OF INVENTION: DEVICES
; FILE REFERENCE: C1005/7012/KA/ERG
; CURRENT APPLICATION NUMBER: US/09/574,749B
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
; US-09-344-040C-122
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Homo Sapiens source
;
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us-09-574-749B-35.

Query Match 57.9%; Score 33; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.1e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLMWIT 6
 |||||
 Db 4 LLMWIT 9

RESULT 15
 US-10-177-277-122
 ; Sequence 122, Application US/10177277
 ; GENERAL INFORMATION:
 ; APPLICANT: Tureci, Ozlem
 ; APPLICANT: Sahin, Ugur
 ; APPLICANT: Pfreundschuh, Michael
 ; APPLICANT: Ramensee, Hans Georg
 ; APPLICANT: Stevanovic, Stefan
 ; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determining Expression of an SSX Gene, Peptides Derived From Said SSX Gene
 ; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
 ; TITLE OF INVENTION: Gene, and uses Thereof
 ; FILE REFERENCE: LUD 5556.1
 ; CURRENT APPLICATION NUMBER: US/10/177,277
 ; CURRENT FILING DATE: 2002-06-21
 ; PRIOR APPLICATION NUMBER: US/09/344,040
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: US 09/105,839
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 08/851,130
 ; PRIOR FILING DATE: 1997-05-05
 ; NUMBER OF SEQ ID NOS: 132
 ; SEQ ID NO 122
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-177-277-122

Query Match 57.9%; Score 33; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 3.1e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLMWIT 6
 |||||
 Db 4 LLMWIT 9

Search completed: July 16, 2002, 08:03:20
 Job time: 198 sec

SUMMARIES							
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1	57	100.0	10	4	US-09-359-503-7	Sequence 7, Appli	
2	47	82.5	9	4	US-09-183-931-43	Sequence 43, Appli	
3	47	82.5	9	4	US-09-359-503-5	Sequence 5, Appli	
4	47	82.5	9	4	US-09-062-422-5	Sequence 5, Appli	
5	47	82.5	9	4	US-08-937-263B-5	Sequence 50, Appli	
6	47	82.5	9	4	US-09-166-448-80	Sequence 80, Appli	
7	33	57.9	6	4	US-09-359-503-14	Sequence 14, Appli	
8	33	57.9	6	4	US-09-062-422-7	Sequence 7, Appli	
9	33	57.9	6	4	US-08-937-263B-7	Sequence 7, Appli	
10	33	57.9	9	4	US-09-183-931-44	Sequence 44, Appli	
11	33	57.9	9	4	US-09-359-503-6	Sequence 6, Appli	
12	33	57.9	9	4	US-09-062-422-6	Sequence 6, Appli	
13	33	57.9	9	4	US-08-937-263B-6	Sequence 6, Appli	
14	33	57.9	9	4	US-09-166-448-81	Sequence 81, Appli	
15	27	47.4	8	4	US-09-020-065A-24	Sequence 24, Appli	
16	26	45.6	6	2	US-08-482-228-186	Sequence 186, Appli	
17	26	45.6	6	3	US-08-482-528-186	Sequence 186, Appli	
18	26	45.6	6	3	US-08-937-263B-15	Sequence 35, Appli	
19	25	43.9	9	1	US-08-484-044-7	Sequence 7, Appli	
20	25	43.9	10	3	US-08-768-859A-15	Sequence 15, Appli	
21	25	43.9	10	3	US-08-767-820A-15	Sequence 15, Appli	
22	25	43.9	10	5	PCT-US95-06157-15	Sequence 15, Appli	
23	24	42.1	10	4	US-08-379-580-6	Sequence 6, Appli	
24	23	40.4	6	1	US-07-620-426B-2	Sequence 2, Appli	
25	23	40.4	6	1	US-07-662-007B-2	Sequence 2, Appli	
26	23	40.4	6	1	US-07-824-247-2	Sequence 2, Appli	
27	23	40.4	6	3	US-08-470-204A-2	Sequence 2, Appli	

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OM protein - protein search, using sw model

Run on: July 16, 2002, 07:56:42 ; Search time 15.68 Seconds
(without alignments)
15.578 Million cell updates/sec

Title: US-09-165-546A-7
Perfect score: 57
Sequence: 1 LLMWITQCF1L 10

Scoring table: BLOSUM62
Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 70601

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
US-09-359-503-7
; Sequence 7, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Method for Determining Antibodies
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, NO. 6251603man D.
; REGISTRATION NUMBER: 30,946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
 US-09-359-503-7

Query Match 100.0%; Score 57; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQCF1 10
 Db 1 LLMWITQCF1 10

RESULT 2
 US-09-183-931-43
 ; Sequence 43, Application US/09183931C
 ; Patent No. 6210886
 ; GENERAL INFORMATION:
 ; APPLICANT: Van Baren, Nicolas
 ; APPLICANT: Brasseur, Francis
 ; APPLICANT: Boon-Falleur, Thierry
 ; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
 ; FILE REFERENCE: LUD 5527.1-JEL/ES
 ; CURRENT APPLICATION NUMBER: US/09/183,931C
 ; CURRENT FILING DATE: 2000-02-28
 ; EARLIER APPLICATION NUMBER: US 09/018,422
 ; EARLIER FILING DATE: 1998 - 02 - 04
 ; SEQ ID NO 43
 ; NUMBER OF SEQ ID NOS: 4 4
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION:
 ; US-09-183-931-43

Query Match 82.5%; Score 47; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQ1 8
 Db 2 LLMWITQ1 9

RESULT 3
 US-09-359-503-5
 ; Sequence 5, Application US/09359503
 ; Patent No. 6251603
 ; GENERAL INFORMATION:
 ; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
 ; APPLICANT: Knuth, Alexander
 ; TITLE OF INVENTION: Method for Determining Status of A
 ; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
 ; TITLE OF INVENTION: a Patient Sample
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski, L.L.P.
 ; STREET: 666 Fifth Avenue
 ; CITY: New York City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10103

Computer readable form:
 Medium type: Diskette, 3.5 inch, 144 kb storage
 Computer: IBM
 Operating system: PC-DOS
 Software: WordPerfect

Current application data:
 Application number: US/09/359,503
 Filing date: July 23, 1999

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/165,546
 FILING DATE: October 2, 1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/062,422
 FILING DATE: April 17, 1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/937,263
 FILING DATE: September 15, 1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/752,182
 FILING DATE: 03-October-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 6251603man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5466.1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-3000
 TELEFAX: (212) 752-5958
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-09-359-503-5

Query Match 82.5%; Score 47; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLMWITQC 8
 Db 2 LLMWITQC 9

RESULT 4
 US-09-062-422-5
 ; Sequence 5, Application US/09062422
 ; Patent No. 6252052
 ; GENERAL INFORMATION:
 ; APPLICANT: Stockert, Elisabeth; Jager, Elke;
 ; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
 ; APPLICANT: Old, Lloyd J.
 ; TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
 ; TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
 ; TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
 ; TITLE OF INVENTION: THEREFROM
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felte & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WordPerfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/062,422
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/937,263
 ; FILING DATE: September 15, 1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/752,182
 ; FILING DATE: 03-October-1996
 ; ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6252052man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5466.3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 838-3884
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-09-062-422-5

Query Match 82.5%; Score 47; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
 Db 2 LLMWITQC 9

RESULT 5
 US-08-937-263B-5
 ; Sequence 5, Application US/08937263B
 ; Patent No. 6274145

GENERAL INFORMATION:
 APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
 APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
 APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
 TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
 ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
 TITLE OF INVENTION: ITSELF, AND USES THEREOF
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fulbright & Jaworski, L.L.P.
 STREET: 666 Fifth Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10103

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/937,263B
 FILING DATE: September 15, 1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/725,182
 FILING DATE: October 3, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Sinn, Eric, Patent Agent
 REGISTRATION NUMBER: 40,177

REFERENCE/DOCKET NUMBER: LUD 5466.1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-3000
 TELEFAX: (212) 752-5958
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-937-263B-5

Query Match 82.5%; Score 47; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8

RESULT 6
 US-09-166-448-80
 ; Sequence 80, Application US/09166448
 ; Patent No. 6291430
 ; GENERAL INFORMATION:
 ; APPLICANT: Chaux, Pascal
 ; APPLICANT: Vantomme, Valrie
 ; APPLICANT: Stroobant, Vincent
 ; APPLICANT: Boon-Falleur, Thierry
 ; APPLICANT: van der Bruggen, Pierre
 ; APPLICANT: Thielemans, Kris
 ; APPLICANT: Corthals, Jurgen
 ; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
 ; FILE REFERENCE: L0461/7052
 ; CURRENT APPLICATION NUMBER: US/09/166,448
 ; CURRENT FILING DATE: 1998-10-05
 ; NUMBER OF SEQ ID NOS: 81
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 80
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-166-448-80

Query Match 82.5%; Score 47; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8
 Db 2 LLMWITQC 9

RESULT 7
 US-09-359-503-14
 ; Sequence 14, Application US/09359503
 ; Patent No. 6251603
 ; GENERAL INFORMATION:
 ; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
 ; APPLICANT: Knuth, alexander
 ; TITLE OF INVENTION: Method for Determining Status Of A
 ; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
 ; TITLE OF INVENTION: a Patient Sample
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski, L.L.P.
 ; STREET: 666 Fifth Avenue
 ; CITY: New York City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WordPerfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/937,263B
 ; FILING DATE: September 15, 1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/725,182
 ; FILING DATE: October 3, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sinn, Eric, Patent Agent
 ; REGISTRATION NUMBER: 40,177
 ; REFERENCE/DOCKET NUMBER: LUD 5466.1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 318-3000
 ; TELEFAX: (212) 752-5958
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-09-359-503-14

Query Match 82.5%; Score 47; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8

RESULT 8
 US-09-165-546
 ; Sequence 165, Application US/09165,546
 ; Patent No. 6251603
 ; GENERAL INFORMATION:
 ; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
 ; APPLICANT: Knuth, alexander
 ; TITLE OF INVENTION: Method for Determining Status Of A
 ; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
 ; TITLE OF INVENTION: a Patient Sample
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski, L.L.P.
 ; STREET: 666 Fifth Avenue
 ; CITY: New York City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WordPerfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/359,503
 ; FILING DATE: July 23, 1999
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/165,546
 ; FILING DATE: October 2, 1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/062,422
 ; FILING DATE: April 17, 1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/937,263

Query Match 82.5%; Score 47; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWITQC 8

FILING DATE: September 15, 1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/752,182
 FILING DATE: 03-October-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 6251603man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5466.1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-3000
 TELEFAX: (212) 752-5958
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-09-359-503-14

RESULT 9
 US-08-937-263B-7
 ; Sequence 7, Application US/08937263B
 ; Patent No. 6274145

; GENERAL INFORMATION:
 ; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
 ; APPLICANT: Cure, Ali; Old, Lloyd J.; Jager, Elke;
 ; APPLICANT: Knuth; Drijfhout, Jan W.
 ; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
 ; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
 ; TITLE OF INVENTION: ITSELF, AND USES THEREOF
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski, L.L.P.
 ; STREET: 666 Fifth Avenue
 ; CITY: New York City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10103

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WordPerfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/937,263B
 ; FILING DATE: September 15, 1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/725,182
 ; FILING DATE: October 3, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sinn, Eric, Patent Agent
 ; REGISTRATION NUMBER: 40,177
 ; REFERENCE/DOCKET NUMBER: LUD 5466.1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 318-3000
 ; TELEFAX: (212) 752-5958
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-08-937-263B-7

Query Match 57.9%; Score 33; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 US-09-062-422-7
 ; Sequence 7, Application US/09062422
 ; Patent No. 6252052

; GENERAL INFORMATION:
 ; APPLICANT: Stockert, Elisabeth; Jager, Elke;
 ; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
 ; APPLICANT: Old, Lloyd J.
 ; TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
 ; TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
 ; TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
 ; TITLE OF INVENTION: THEREFROM
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WordPerfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/062,422
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/937,263
 ; FILING DATE: September 15, 1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/752,182
 ; FILING DATE: 03-October-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hanson, No. 6252052man D.
 ; REGISTRATION NUMBER: 30,946
 ; REFERENCE/DOCKET NUMBER: LUD 5466.3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 688-9200
 ; TELEFAX: (212) 838-3884
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6 amino acids

Query Match 57.9%; Score 33; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
 US-09-183-931-44
 ; Sequence 44, Application US/09183931C
 ; Patent No. 6210886
 ; GENERAL INFORMATION:

APPLICANT: Van Baren, Nicolas
 APPLICANT: Brasseur, Francis
 APPLICANT: Boon-Falleur, Thierry
 TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
 TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
 FILE REFERENCE: LUD 5527.1-JEL/ES
 CURRENT APPLICATION NUMBER: US/09/183,931C
 CURRENT FILING DATE: 2000-02-28
 EARLIER APPLICATION NUMBER: US 09/018,422
 NUMBER OF SEQ ID NOS: 44
 SEQ ID NO 44
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION:
 US-09-183-931-44

Query Match 57.9%; Score 33; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 6; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

RESULT 12
 US-09-062-422-6
 Sequence 6, Application US/09062422
 ; Patent No. 6252052
 ; GENERAL INFORMATION:
 ; APPLICANT: Stockert, Elisabeth; Jager, Elke;
 ; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
 ; APPLICANT: Old, Lloyd J.
 ; TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
 ; TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
 ; TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
 ; TITLE OF INVENTION: THEREFROM
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felife & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WordPerfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/752,182
 ; FILING DATE: 03-October-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hanson, No. 6252052man D.
 ; REGISTRATION NUMBER: 30, 946
 ; REFERENCE/DOCKET NUMBER: LUD 5466.3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 688-9200
 ; TELEFAX: (212) 838-3884
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; TOPOLogy: linear
 ; US-09-062-422-6

Query Match 57.9%; Score 33; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 6; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

APPLICANT: Van Baren, Nicolas
 APPLICANT: Brasseur, Francis
 APPLICANT: Boon-Falleur, Thierry
 TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
 TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
 FILE REFERENCE: LUD 5527.1-JEL/ES
 CURRENT APPLICATION NUMBER: US/09/183,931C
 CURRENT FILING DATE: 2000-02-28
 EARLIER APPLICATION NUMBER: US 09/018,422
 NUMBER OF SEQ ID NOS: 44
 SEQ ID NO 44
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION:
 US-09-183-931-44

Query Match 57.9%; Score 33; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 6; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

APPLICANT: Van Baren, Nicolas
 APPLICANT: Brasseur, Francis
 APPLICANT: Boon-Falleur, Thierry
 TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
 TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
 FILE REFERENCE: LUD 5527.1-JEL/ES
 CURRENT APPLICATION NUMBER: US/09/183,931C
 CURRENT FILING DATE: 2000-02-28
 EARLIER APPLICATION NUMBER: US 09/018,422
 NUMBER OF SEQ ID NOS: 44
 SEQ ID NO 44
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION:
 US-09-183-931-44

Query Match 57.9%; Score 33; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 6; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 LLMWIT 6 ; CURRENT APPLICATION NUMBER: US/09/166,448
 Db 4 LLMWIT 9 ; CURRENT FILING DATE: 1998-10-05
 ; NUMBER OF SEQ ID NOS: 81
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 81
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-166-448-81

RESULT 13
 US-08-937-263B-6
 ; Sequence 6, Application US/08937263B
 ; Patent No. 6274145
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
 ; Gure, Ali; Old, Lloyd J.; Jager, Elke;
 ;
 ; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
 ;
 ; TITLE OF INVENTION: ISOLATED NUCLEAR ACID MOLECULE
 ;
 ; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
 ;
 ; TITLE OF INVENTION: ITSELF, AND USES THEREOF
 ;
 ; NUMBER OF SEQUENCES: 8
 ;
 ; CORRESPONDENCE ADDRESS:
 ;
 ; ADDRESSEE: Fulbright & Jaworski, L.L.P.
 ; STREET: 666 Fifth Avenue
 ; CITY: New York City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: WordPerfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/937,263B
 ; FILING DATE: September 15, 1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/725,182
 ; FILING DATE: October 3, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sinn, Eric, Patent Agent
 ; REGISTRATION NUMBER: 40,177
 ; REFERENCE/DOCKET NUMBER: IUD 5466.1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 318-3000
 ; TELEFAX: (212) 752-5958
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-08-937-263B-6

Query Match 57.9%; Score 33; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLMWIT 6
 Db 4 LLMWIT 9

RESULT 15
 US-09-020-065A-24
 ; Sequence 24, Application US/09020065A
 ; Patent No. 6346602
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Townsend, Robert M.
 ; APPLICANT: Krongold, Robert
 ; TITLE OF INVENTION: Peptide Mimics of the Cytokine Receptor Common
 ;
 ; TITLE OF INVENTION: Gamma Chain and Methods and Compositions for
 ;
 ; TITLE OF INVENTION: Making and Using the Same
 ;
 ; NUMBER OF SEQUENCES: 37
 ;
 ; CORRESPONDENCE ADDRESS:
 ;
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6346602ris LLP
 ; STREET: One Liberty Place, 46th Floor
 ; CITY: Philadelphia
 ; STATE: Pennsylvania
 ; COUNTRY: USA
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows NT
 ; SOFTWARE: Wordperfect V. 8
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/020,065A
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ;
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/036,941
 ; FILING DATE: 07-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: DeLuca, Mark
 ; REGISTRATION NUMBER: 33,229
 ; REFERENCE/DOCKET NUMBER: TJu-2291
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-568-3100
 ; TELEFAX: 215-568-3439
 ; INFORMATION FOR SEQ ID NO: 24:
 ;
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: peptide
 ; US-09-020-065A-24

Query Match 47.4%; Score 27; DB 4; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.7e+05;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LMMWITQC 8
 Db 2 QYLITQC 8

RESULT 14
 US-09-166-448-81
 ; Sequence 81, Application US/09166448
 ; Patent No. 6291430
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Chaux, Pascal
 ; APPLICANT: Vantomme, Valarie
 ; APPLICANT: Stroobant, Vincent
 ; APPLICANT: Boon-Falleur, Thierry
 ; APPLICANT: van der Bruggen, Pierre
 ; APPLICANT: Thielmans, Kris
 ; APPLICANT: Corthals, Jurgen
 ; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
 ; FILE REFERENCE: L0461/7052

Search completed: July 16, 2002, 08:02:06
Job time: 324 sec